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SEQUENCE LISTING

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<120> GLYPHOSATE TOLERANT 5-ENOLPYRUVYL SHIKIMATE-3-PHOSPHATE SYNTHASES

<130> 11899.0175.CNUS01 MOBT:175-2

<140> 09/464,099

<141> 1999-12-16

<150> US 09/137,440

<151> 1998-08-20

<150> US 08/833,485

<151> 1997-04-07

<150> US 08/306,063

<151> 1994-09-13

<150> US 07/749,611

<151> 1991-08-28

<150> US 07/576,537

<151> 1990-08-31

<160> 70

<170> PatentIn version 3.0

<210> 1

<211> 597

<212> DNA

<213> Figwort mosaic virus

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aggaagaatt ctcagtccaa agcctcaaca aggtcagggc acagagtctc caaaccattt 180

gccaaaagct acaggagatc aatgaagaat cttcaatcaa agtaaactac tggccagca 240

catgcatcat ggtcagtaag tttcagaaaa agacatccac cgaagactta aagtttagtgg 300

gcatcttga aagtaatctt gtcaacatcg agcagctggc ttgtggggac cagacaaaaaa 360

aggaatggtg cagaattgtt aggcgcacct accaaaagca tctttgcctt tattgcaaag 420

ataaaaggcaga ttccctcttagt acaagtgggg aacaaaataa cgtggaaaag agctgtcctg 480

1
108

F

acagcccaact cactaatgcg tatgacgaac gcagtgcgca ccacaaaaga attccctcta 540
 tataagaagg cattcattcc catttgaagg atcatcagat actaaccaat atttctc 597

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 <212> DNA
 <213> Agrobacterium sp.

<220>
 <221> CDS
 <222> (62) .. (1426)

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c atg tcg cac ggt gca agc agc cgg ccc gca acc gcc cgc aaa tcc tct 109
 Met Ser His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
 1 5 10 15

ggc ctt tcc gga acc gtc cgc att ccc ggc gac aag tcg atc tcc cac 157
 Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
 20 25 30

cggtcc ttc atg ttc ggc ggt ctc gcg agc ggt gaa acg cgc atc acc 205
 Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
 35 40 45

ggc ctt ctg gaa ggc gag gac gtc atc aat acg ggc aag gcc atg cag 253
 Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
 50 55 60

gcc atg ggc gcc agg atc cgt aag gaa ggc gac acc tgg atc atc gat 301
 Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
 65 70 75 80

ggc gtc ggc aat ggc ggc ctc ctg gcg cct gag ggc ccg ctc gat ttc 349
 Gly Val Gly Asn Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
 85 90 95

ggc aat gcc gcc acg ggc tgc cgc ctg acc atg ggc ctc gtc ggg gtc 397
 Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val
 100 105 110

tac gat ttc gac agc acc ttc atc ggc gac gcc tcg ctc aca aag cgc 445
 Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
 115 120 125

ccg atg ggc cgc gtg ttg aac ccg ctg cgc gaa atg ggc gtg cag gtg 493
 Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
 130 135 140

aaa tcg gaa gac ggt gac cgt ctt ccc gtt acc ttg cgc ggg ccg aag Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys 145 150 155 160	541
acg ccg acg ccg atc acc tac cgc gtg ccg atg gcc tcc gca cag gtg Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val 165 170 175	589
aag tcc gcc gtg ctg ctc gcc ggc ctc aac acg ccc ggc atc acg acg Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr 180 185 190	637
gtc atc gag ccg atc atg acg cgc gat cat acg gaa aag atg ctg cag Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln 195 200 205	685
ggc ttt ggc gcc aac ctt acc gtc gag acg gat gcg gac ggc gtg cgc Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val Arg 210 215 220	733
acc atc cgc ctg gaa ggc cgc ggc aag ctc acc ggc caa gtc atc gac Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp 225 230 235 240	781
gtg ccg ggc gac ccg tcc tcg acg gcc ttc ccg ctg gtt gcg gcc ctg Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu 245 250 255	829
ctt gtt ccg ggc tcc gac gtc acc atc ctc aac gtg ctg atg aac ccc Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro 260 265 270	877
acc cgc acc ggc ctc atc ctg acg ctg cag gaa atg ggc gcc gac atc Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile 275 280 285	925
gaa gtc atc aac ccg cgc ctt gcc ggc ggc gaa gac gtg gcg gac ctg Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu 290 295 300	973
cgc gtt cgc tcc tcc acg ctg aag ggc gtc acg gtg ccg gaa gac cgc Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg 305 310 315 320	1021
gcg cct tcg atg atc gac gaa tat ccg att ctc gct gtc gcc gcc gcc Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala 325 330 335	1069
ttc gcg gaa ggg gcg acc gtg atg aac ggt ctg gaa gaa ctc cgc gtc Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val 340 345 350	1117
aag gaa agc gac cgc ctc tcg gcc gtc gcc aat ggc ctc aag ctc aat Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn	1165

355

360

365

ggc gtg gat tgc gat gag ggc gag acg tcg ctc gtc gtg cgc ggc cgc	370	375	380	1213
Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg				
cct gac ggc aag ggg ctc ggc aac gcc tcg ggc gcc gcc gtc gcc acc	385	390	395	1261
Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr				
cat ctc gat cac cgc atc gcc atg agc ttc ctc gtc atg ggc ctc gtg	405	410	415	1309
His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val				
tcg gaa aac cct gtc acg gtg gac gat gcc acg atg atc gcc acg agc	420	425	430	1357
Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser				
ttc ccg gag ttc atg gac ctg atg gcc ggg ctg ggc gcg aag atc gaa	435	440	445	1405
Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu				
ctc tcc gat acg aag gct gcc tgatgacctt cacaatcgcc atcgatggtc	450	455		1456
Leu Ser Asp Thr Lys Ala Ala				
ccgctgcggc cggcaagggg acgctctcgcc gccgtatcgcc ggaggtctat ggctttcatc				1516
atctcgatac gggcctgacc tatcgccca cggccaaagc gctgctcgat cgccggctgt				1576
cgcttcatga cgaggcgggtt gcggccgatg tcgcccgc aa tctcgatctt gccgggctcg				1636
accggtcggt gctgtcggcc catgccccatcg gcgaggcggc ttcaagatc gcggtcatgc				1696
cctcggtcg gcccccgctg gtcgaggcgc agcgcagctt tgcggcgcgt gagccggca				1756
cgggtctggc tggacgcgat atcggcacgg tggctgccc ggatgcgcg gtgaagctct				1816
atgtcaccgc gtcaccggaa gtgcgcgcga aacgcgccta tgacaaatc ctcggcaatg				1876
gcgggttggc cgattacggg acgatcctcg agatatccg ccgcgcgcgac gagcgggaca				1936
tgggtcgggc ggacagtcc ttgaagcccg ccgacgatgc gcactt				1982

<210> 3

<211> 455

<212> PRT

<213> Agrobacterium sp.

<400> 3

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20 25 30

Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
35 40 45

Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
50 55 60

Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
65 70 75 80

Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
85 90 95

Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val
100 105 110

Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
115 120 125

Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
130 135 140

Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys
145 150 155 160

Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
165 170 175

Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr
180 185 190

Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
195 200 205

Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val Arg
210 215 220

Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp
225 230 235 240

Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
245 250 255

Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro
260 265 270

Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
275 280 285

Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
290 295 300

Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg
305 310 315 320

Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala
325 330 335

Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val
340 345 350

Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn
355 360 365

Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg
370 375 380

Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr
385 390 395 400

His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
405 410 415

Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
420 425 430

Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
435 440 445

Leu Ser Asp Thr Lys Ala Ala
450 455

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<212> DNA
<213> Agrobacterium sp.

<220>
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<222> (86) .. (1432)

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gccaaaatgt gactgtgaaa aatcc atg tcc cat tct gca tcc ccg aaa cca 112
Met Ser His Ser Ala Ser Pro Lys Pro
1 5
gca acc gcc cgc tcg gag gca ctc acg ggc gaa atc cgc att ccg 160
Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg Ile Pro
10 15 20 25
ggc gac aag tcc atc tcg cat cgc tcc ttc atg ttt ggc ggt ctc gca 208
Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu Ala
30 35 40
tcg ggc gaa acc cgc atc acc ggc ctt ctg gaa ggc gag gac gtc atc 256
Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile
45 50 55
aat aca ggc cgc gcc atg cag gcc atg ggc gcg aaa atc cgt aaa gag 304
Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg Lys Glu
60 65 70
ggc gat gtc tgg atc atc aac ggc gtc ggc aat ggc tgc ctg ttg cag 352
Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu Leu Gln
75 80 85
ccc gaa gct gcg ctc gat ttc ggc aat gcc gga acc ggc gcg cgc ctc 400
Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala Arg Leu
90 95 100 105
acc atg ggc ctt gtc ggc acc tat gac atg aag acc tcc ttt atc ggc 448
Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe Ile Gly
110 115 120
gac gcc tcg ctg tcg aag cgc ccg atg ggc cgc gtg ctg aac ccg ttg 496
Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn Pro Leu
125 130 135

cgc gaa atg ggc gtt cag gtg gaa gca gcc gat ggc gac cgc atg ccg Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg Met Pro 140	145	150	544	
ctg acg ctg atc ggc ccg aag acg gcc aat ccg atc acc tat cgc gtg Leu Thr Leu Ile Gly Pro Lys Thr Ala Asn Pro Ile Thr Tyr Arg Val 155	160	165	592	
ccg atg gcc tcc gcg cag gta aaa tcc gcc gtg ctg ctc gcc ggt ctc Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala Gly Leu 170	175	180	185	640
aac acg ccg ggc gtc acc acc gtc atc gag ccg gtc atg acc cgc gac Asn Thr Pro Gly Val Thr Val Ile Glu Pro Val Met Thr Arg Asp 190	195	200	688	
cac acc gaa aag atg ctg cag ggc ttt ggc gcc gac ctc acg gtc gag His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr Val Glu 205	210	215	736	
acc gac aag gat ggc gtg cgc cat atc cgc atc acc ggc cag ggc aag Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln Gly Lys 220	225	230	784	
ctt gtc ggc cag acc atc gac gtg ccg ggc gat ccg tca tcg acc gcc Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser Thr Ala 235	240	245	832	
tcc ccg ctc gtt gcc gcc ctt ctg gtg gaa ggt tcc gac gtc acc atc Phe Pro Leu Val Ala Ala Leu Val Glu Gly Ser Asp Val Thr Ile 250	255	260	265	880
cgc aac gtg ctg atg aac ccg acc cgt acc ggc ctc atc ctc acc ttg Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu Thr Leu 270	275	280	928	
cag gaa atg ggc gcc gat atc gaa gtg ctc aat gcc cgt ctt gca ggc Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu Ala Gly 285	290	295	976	
ggc gaa gac gtc gcc gat ctg cgc gtc agg gct tcg aag ctc aag ggc Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu Lys Gly 300	305	310	1024	
gtc gtc gtt ccg ccg gaa cgt gcg ccg tcg atg atc gac gaa tat ccg Val Val Val Pro Pro Glu Arg Ala Pro Ser Met Ile Asp Glu Tyr Pro 315	320	325	1072	
gtc ctg gcg att gcc gcc tcc ttc gcg gaa ggc gaa acc gtg atg gac Val Leu Ala Ile Ala Ala Ser Phe Ala Glu Gly Glu Thr Val Met Asp 330	335	340	345	1120
ggg ctc gac gaa ctg cgc gtc aag gaa tcg gat cgt ctg gca gcg gtc Gly Leu Asp Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Val			1168	

350	355	360	
gca cgc ggc ctt gaa gcc aac ggc gtc gat tgc acc gaa ggc gag atg Ala Arg Gly Leu Glu Ala Asn Gly Val Asp Cys Thr Glu Gly Glu Met			1216
365	370	375	
tcg ctg acg gtt cgc ggc cgc ccc gac ggc aag gga ctg ggc ggc ggc Ser Leu Thr Val Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly Gly			1264
380	385	390	
acg gtt gca acc cat ctc gat cat cgt atc gcg atg agc ttc ctc gtg Thr Val Ala Thr His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val			1312
395	400	405	
atg ggc ctt gcg gcg gaa aag ccg gtg acg gtt gac gac agt aac atg Met Gly Leu Ala Ala Glu Lys Pro Val Thr Val Asp Asp Ser Asn Met			1360
410	415	420	425
atc gcc acg tcc ttc ccc gaa ttc atg gac atg ccg gga ttg ggc Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly Leu Gly			1408
430	435	440	
gca aag atc gag ttg agc ata ctc tagtcactcg acagcgaaaa tattatttgc Ala Lys Ile Glu Leu Ser Ile Leu			1462
445			
gagattgggc attattaccc gttggctctca gcgggggttt aatgtccaat cttccatacg			1522
taacagcatc aggaaatatc aaaaaagctt tagaaggaat tgctagagca gcgacgcccgc			1582
ctaagctttc tcaagacttc gttaaaactg tactgaaatc ccggggggtc cggggatcaa			1642
atgacttcat ttctgagaaa ttggcctcgc a			1673

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 <211> 449
 <212> PRT
 <213> Agrobacterium sp.

<400> 5

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Ala	Leu	Thr	Gly	Glu	Ile	Arg	Ile	Pro	Gly	Asp	Lys	Ser	Ile	Ser	His
					20			25					30		

Arg	Ser	Phe	Met	Phe	Gly	Gly	Leu	Ala	Ser	Gly	Glu	Thr	Arg	Ile	Thr
							35		40			45			

110

F

Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Arg Ala Met Gln
50 55 60

Ala Met Gly Ala Lys Ile Arg Lys Glu Gly Asp Val Trp Ile Ile Asn
65 70 75 80

Gly Val Gly Asn Gly Cys Leu Leu Gln Pro Glu Ala Ala Leu Asp Phe
85 90 95

Gly Asn Ala Gly Thr Gly Ala Arg Leu Thr Met Gly Leu Val Gly Thr
100 105 110

Tyr Asp Met Lys Thr Ser Phe Ile Gly Asp Ala Ser Leu Ser Lys Arg
115 120 125

Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
130 135 140

Glu Ala Ala Asp Gly Asp Arg Met Pro Leu Thr Leu Ile Gly Pro Lys
145 150 155 160

Thr Ala Asn Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
165 170 175

Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Val Thr Thr
180 185 190

Val Ile Glu Pro Val Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
195 200 205

Gly Phe Gly Ala Asp Leu Thr Val Glu Thr Asp Lys Asp Gly Val Arg
210 215 220

His Ile Arg Ile Thr Gly Gln Gly Lys Leu Val Gly Gln Thr Ile Asp
225 230 235 240

Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
245 250 255

Leu Val Glu Gly Ser Asp Val Thr Ile Arg Asn Val Leu Met Asn Pro
260 265 270

10
11/11

F

Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
275 280 285

Glu Val Leu Asn Ala Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
290 295 300

Arg Val Arg Ala Ser Lys Leu Lys Gly Val Val Val Pro Pro Glu Arg
305 310 315 320

Ala Pro Ser Met Ile Asp Glu Tyr Pro Val Leu Ala Ile Ala Ala Ser
325 330 335

Phe Ala Glu Gly Glu Thr Val Met Asp Gly Leu Asp Glu Leu Arg Val
340 345 350

Lys Glu Ser Asp Arg Leu Ala Ala Val Ala Arg Gly Leu Glu Ala Asn
355 360 365

Gly Val Asp Cys Thr Glu Gly Glu Met Ser Leu Thr Val Arg Gly Arg
370 375 380

Pro Asp Gly Lys Gly Leu Gly Gly Thr Val Ala Thr His Leu Asp
385 390 395 400

His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Ala Ala Glu Lys
405 410 415

Pro Val Thr Val Asp Asp Ser Asn Met Ile Ala Thr Ser Phe Pro Glu
420 425 430

Phe Met Asp Met Met Pro Gly Leu Gly Ala Lys Ile Glu Leu Ser Ile
435 440 445

Leu

<210> 6
<211> 1500
<212> DNA
<213> Pseudomonas sp.

<220>
<221> CDS
<222> (34)..(1380)

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Lys Pro Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg
10 15 20

att ccg ggc gac aag tcc atc tcg cat cgc tcc ttc atg ttt ggc ggt 150
Ile Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly
25 30 35

ctc gca tcg ggc gaa acc cgc atc acc ggc ctt ctg gaa ggc gag gac 198
Leu Ala Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp
40 45 50 55

gtc atc aat aca ggc cgc gcc atg cag gcc atg ggc gcg aaa atc cgt 246
Val Ile Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg
60 65 70

aaa gag ggc gat gtc tgg atc atc aac ggc gtc ggc aat ggc tgc ctg 294
Lys Glu Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu
75 80 85

ttg cag ccc gaa gct gcg ctc gat ttc ggc aat gcc gga acc ggc gcg 342
Leu Gln Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala
90 95 100

cgc ctc acc atg ggc ctt gtc ggc acc tat gac atg aag acc tcc ttt 390
Arg Leu Thr Met Gly Leu Val Gly Thr Tyr Asp Met Lys Thr Ser Phe
105 110 115

atc ggc gac gcc tcg ctg tcg aag cgc ccg atg ggc cgc gtg ctg aac 438
Ile Gly Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu Asn
120 125 130 135

ccg ttg cgc gaa atg ggc gtt cag gtg gaa gca gcc gat ggc gac cgc 486
Pro Leu Arg Glu Met Gly Val Gln Val Glu Ala Ala Asp Gly Asp Arg
140 145 150

atg ccg ctg acg ctg atc ggc ccg aag acg gcc aat ccg atc acc tat 534
Met Pro Leu Thr Leu Ile Gly Pro Lys Thr Ala Asn Pro Ile Thr Tyr
155 160 165

cgc gtg ccg atg gcc tcc gcg cag gta aaa tcc gcc gtg ctg ctc gcc 582
Arg Val Pro Met Ala Ser Ala Gln Val Lys Ser Ala Val Leu Leu Ala
170 175 180

ggt ctc aac acg ccg ggc gtc acc acc gtc atc gag ccg gtc atg acc		630	
Gly Leu Asn Thr Pro Gly Val Thr Thr Val Ile Glu Pro Val Met Thr			
185	190	195	
cgc gac cac acc gaa aag atg ctg cag ggc ttt ggc gcc gac ctc acg		678	
Arg Asp His Thr Glu Lys Met Leu Gln Gly Phe Gly Ala Asp Leu Thr			
200	205	210	215
gtc gag acc gac aag gat ggc gtg cgc cat atc cgc atc acc ggc cag		726	
Val Glu Thr Asp Lys Asp Gly Val Arg His Ile Arg Ile Thr Gly Gln			
220	225	230	
ggc aag ctt gtc ggc cag acc atc gac gtg ccg ggc gat ccg tca tcg		774	
Gly Lys Leu Val Gly Gln Thr Ile Asp Val Pro Gly Asp Pro Ser Ser			
235	240	245	
acc gcc ttc ccg ctc gtt gcc gcc ctt ctg gtg gaa ggt tcc gac gtc		822	
Thr Ala Phe Pro Leu Val Ala Ala Leu Leu Val Glu Gly Ser Asp Val			
250	255	260	
acc atc cgc aac gtg ctg atg aac ccg acc cgt acc ggc ctc atc ctc		870	
Thr Ile Arg Asn Val Leu Met Asn Pro Thr Arg Thr Gly Leu Ile Leu			
265	270	275	
acc ttg cag gaa atg ggc gcc gat atc gaa gtg ctc aat gcc cgt ctt		918	
Thr Leu Gln Glu Met Gly Ala Asp Ile Glu Val Leu Asn Ala Arg Leu			
280	285	290	295
gca ggc ggc gaa gac gtc gcc gat ctg cgc gtc agg gct tcg aag ctc		966	
Ala Gly Gly Glu Asp Val Ala Asp Leu Arg Val Arg Ala Ser Lys Leu			
300	305	310	
aag ggc gtc gtc gtt ccg ccg gaa cgt gcg ccg tcg atg atc gac gaa		1014	
Lys Gly Val Val Val Pro Pro Glu Arg Ala Pro Ser Met Ile Asp Glu			
315	320	325	
tat ccg gtc ctg gcg att gcc gcc tcc ttc gcg gaa ggc gaa acc gtc		1062	
Tyr Pro Val Leu Ala Ile Ala Ser Phe Ala Glu Gly Glu Thr Val			
330	335	340	
atg gac ggg ctc gac gaa ctg cgc gtc aag gaa tcg gat cgt ctg gca		1110	
Met Asp Gly Leu Asp Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala			
345	350	355	
gcg gtc gca cgc ggc ctt gaa gcc aac ggc gtc gat tgc acc gaa ggc		1158	
Ala Val Ala Arg Gly Leu Glu Ala Asn Gly Val Asp Cys Thr Glu Gly			
360	365	370	375
gag atg tcg ctg acg gtt cgc ggc cgc ccc gac ggc aag gga ctg ggc		1206	
Glu Met Ser Leu Thr Val Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly			
380	385	390	
ggc ggc acg gtt gca acc cat ctc gat cat cgt atc gcg atg agc ttc		1254	
Gly Gly Thr Val Ala Thr His Leu Asp His Arg Ile Ala Met Ser Phe			



395

400

405

ctc gtg atg ggc ctt gcg gcg gaa aag ccg gtg acg gtt gac gac agt 1302
 Leu Val Met Gly Leu Ala Ala Glu Lys Pro Val Thr Val Asp Asp Ser
 410 415 420

aac atg atc gcc acg tcc ttc ccc gaa ttc atg gac atg atg ccg gga 1350
 Asn Met Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly
 425 430 435

ttg ggc gca aag atc gag ttg agc ata ctc tagtcactcg acagcgaaaa 1400
 Leu Gly Ala Lys Ile Glu Leu Ser Ile Leu
 440 445

tattatttgc gagattgggc attattacgg ttgggtctca gcgggggttt aatgtccat 1460
 cttccatacg taacagcatac aggaaatatac aaaaaagctt 1500

<210> 7
 <211> 449
 <212> PRT
 <213> Pseudomonas sp.

<400> 7

Met Ser His Ser Ala Ser Pro Lys Pro Ala Thr Ala Arg Arg Ser Glu
 1 5 10 15

Ala Leu Thr Gly Glu Ile Arg Ile Pro Gly Asp Lys Ser Ile Ser His
 20 25 30

Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
 35 40 45

Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Arg Ala Met Gln
 50 55 60

Ala Met Gly Ala Lys Ile Arg Lys Glu Gly Asp Val Trp Ile Ile Asn
 65 70 75 80

Gly Val Gly Asn Gly Cys Leu Leu Gln Pro Glu Ala Ala Leu Asp Phe
 85 90 95

Gly Asn Ala Gly Thr Gly Ala Arg Leu Thr Met Gly Leu Val Gly Thr
 100 105 110

14
 21

5

Tyr Asp Met Lys Thr Ser Phe Ile Gly Asp Ala Ser Leu Ser Lys Arg
115 120 125

Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
130 135 140

Glu Ala Ala Asp Gly Asp Arg Met Pro Leu Thr Leu Ile Gly Pro Lys
145 150 155 160

Thr Ala Asn Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
165 170 175

Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Val Thr Thr
180 185 190

Val Ile Glu Pro Val Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
195 200 205

Gly Phe Gly Ala Asp Leu Thr Val Glu Thr Asp Lys Asp Gly Val Arg
210 215 220

His Ile Arg Ile Thr Gly Gln Gly Lys Leu Val Gly Gln Thr Ile Asp
225 230 235 240

Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
245 250 255

Leu Val Glu Gly Ser Asp Val Thr Ile Arg Asn Val Leu Met Asn Pro
260 265 270

Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
275 280 285

Glu Val Leu Asn Ala Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
290 295 300

Arg Val Arg Ala Ser Lys Leu Lys Gly Val Val Val Pro Pro Glu Arg
305 310 315 320

Ala Pro Ser Met Ile Asp Glu Tyr Pro Val Leu Ala Ile Ala Ala Ser
325 330 335

Phe Ala Glu Gly Glu Thr Val Met Asp Gly Leu Asp Glu Leu Arg Val
340 345 350

Lys Glu Ser Asp Arg Leu Ala Ala Val Ala Arg Gly Leu Glu Ala Asn
355 360 365

Gly Val Asp Cys Thr Glu Gly Glu Met Ser Leu Thr Val Arg Gly Arg
370 375 380

Pro Asp Gly Lys Gly Leu Gly Gly Thr Val Ala Thr His Leu Asp
385 390 395 400

His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Ala Ala Glu Lys
405 410 415

Pro Val Thr Val Asp Asp Ser Asn Met Ile Ala Thr Ser Phe Pro Glu
420 425 430

Phe Met Asp Met Met Pro Gly Leu Gly Ala Lys Ile Glu Leu Ser Ile
435 440 445

Leu

<210> 8
<211> 423
<212> PRT
<213> Escherichia coli

<400> 8

Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Thr Ile Asn Leu
1 5 10 15

Pro Gly Ser Lys Thr Val Ser Asn Arg Ala Leu Leu Leu Ala Ala Leu
20 25 30

Ala His Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp Asp Val
35 40 45

Arg His Met Leu Asn Ala Leu Thr Ala Leu Gly Val Ser Tyr Thr Leu
50 55 60

Ser Ala Asp Arg Thr Arg Cys Glu Ile Ile Gly Asn Gly Gly Pro Leu

16
123

F

65

70

75

80

His Ala Glu Gly Ala Leu Glu Leu Phe Leu Gly Asn Ala Gly Thr Ala
85 90 95

Met Arg Pro Leu Ala Ala Ala Leu Cys Leu Gly Ser Asn Asp Ile Val
100 105 110

Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His Leu Val
115 120 125

Asp Ala Leu Arg Leu Gly Gly Ala Lys Ile Thr Tyr Leu Glu Gln Glu
130 135 140

Asn Tyr Pro Pro Leu Arg Leu Gln Gly Gly Phe Thr Gly Gly Asn Val
145 150 155 160

Asp Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu Leu Met
165 170 175

Thr Ala Pro Leu Ala Pro Glu Asp Thr Val Ile Arg Ile Lys Gly Asp
180 185 190

Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met Lys Thr
195 200 205

Phe Gly Val Glu Ile Glu Asn Gln His Tyr Gln Gln Phe Val Val Lys
210 215 220

Gly Gly Gln Ser Tyr Gln Ser Pro Gly Thr Tyr Leu Val Glu Gly Asp
225 230 235 240

Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Ala Ile Lys Gly Gly
245 250 255

Thr Val Lys Val Thr Gly Ile Gly Arg Asn Ser Met Gln Gly Asp Ile
260 265 270

Arg Phe Ala Asp Val Leu Glu Lys Met Gly Ala Thr Ile Cys Trp Gly
275 280 285

Asp Asp Tyr Ile Ser Cys Thr Arg Gly Glu Leu Asn Ala Ile Asp Met
290 295 300

Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr Ala Ala
305 310 315 320

Leu Phe Ala Lys Gly Thr Thr Arg Leu Arg Asn Ile Tyr Asn Trp Arg
325 330 335

Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu Arg Lys
340 345 350

Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile Thr Pro

17
124

F

355

360

365

Pro Glu Lys Leu Asn Phe Ala Glu Ile Ala Thr Tyr Asn Asp His Arg
 370 375 380

Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro Val Thr
 385 390 395 400

Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr Phe Glu
 405 410 415

Gln Leu Ala Arg Ile Ser Gln
 420

<210> 9

<211> 1377

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic

<400> 9

ccatggctca cggtgcaagg agccgtccag caactgctcg taagtcctct ggtctttctg 60

gaaccgtccg tattccaggt gacaagtcta tctcccacag gtccttcatg tttggaggtc 120

tcgctagcgg taaaactcgt atcaccggc ttttggagg tgaagatgtt atcaacactg 180

gtaaggctat gcaagctatg ggtgcagaa tccgtaaagg aggtgatact tggatcattg 240

atgggtttgg taacggtgga ctccttgctc ctgaggctcc tctcgatttc ggtaacgctg 300

caactggttt ccgtttgact atgggtcttgg ttgggttttta cgatttcgat agcactttca 360

ttgggtgacgc ttctctcaact aagcgtccaa tgggtcggtt gttgaaccca cttcgcaaaa 420

tgggtgtgca ggtgaagtct gaagacggtg atcgtcttcc agttaccttgg cgtggaccaa 480

agactccaac gccaatcacc tacagggtaac ctatggcttc cgctcaagtg aagtccgctg 540

ttctgcttgc tggctcaac accccaggtt tcaccactgt tatcgagcca atcatgactc 600

gtgaccacac tggaaaggatg cttcaagggtt ttgggtctaa ccttaccgtt gagactgtatg 660

ctgacgggtt gcttaccatc cgtcttgcgg gtcgtggtaa gctcaccggtaa caagtgttgg 720

atgttccagg tggatccatcc tctactgctt tcccatgggt tgctgccttgc tttgttccagg 780

gttccgacgt caccatcctt aacgttttga tggaaacccaaac ccgtactggtaa ctcatcttgc 840

ctctgcagga aatgggtgccc gacatcgaaag tggatcaaccc acgtcttgcgtt ggtggagaag 900

acgtggctga ctgcgtgtt cgttcttcta ctttgaaggg tggatctgtt ccagaagacc 960

gtgctccttc tatgatcgac gagtatccaa ttctcgctgt tgcagctgca ttgcgtgaag 1020
 gtgctaccgt tatgaacggt ttggaagaac tccgtgttaa ggaaagcgac cgtcttctg 1080
 ctgtcgcaaa cggctctcaag ctcaacggtg ttgattgcga tgaaggtgag acttctctcg 1140
 tcgtgcgtgg tcgtcctgac ggttaagggtc tcggtaacgc ttctggagca gctgtcgcta 1200
 cccacccctcga tcaccgtatc gctatgagct tcctcggttat gggctcggtt tctgaaaacc 1260
 ctgttactgt tcatgtatgct actatgatcg ctactagctt cccagagttc atggatttga 1320
 tggctggtct tggagcttaag atcgaactct ccgacactaa ggctgcttga tgagctc 1377

<210> 10
 <211> 318
 <212> DNA
 <213> *Arabidopsis thaliana*

<220>
 <221> CDS
 <222> (87) .. (317)

<400> 10
 agatctatcg ataagcttga tgtaatttggaa ggaagatcaa aattttcaat cccattttt 60
 cgattgcttc aatttgaagtt tctccg atg gcg caa gtt agc aga atc tgc aat 113
 Met Ala Gln Val Ser Arg Ile Cys Asn
 1 5

ggt gtg cag aac cca tct ctt atc tcc aat ctc tcg aaa tcc agt caa 161
 Gly Val Gln Asn Pro Ser Leu Ile Ser Asn Leu Ser Lys Ser Ser Gln
 10 15 20 25

cgc aaa tct ccc tta tcg gtt tct ctg aag acg cag cag cat cca cga 209
 Arg Lys Ser Pro Leu Ser Val Leu Lys Thr Gln Gln His Pro Arg
 30 35 40

gct tat ccg att tcg tcg tgg gga ttg aag aag agt ggg atg acg 257
 Ala Tyr Pro Ile Ser Ser Trp Gly Leu Lys Ser Gly Met Thr
 45 50 55

tta att ggc tct gag ctt cgt cct ctt aag gtc atg tct tct gtt tcc 305
 Leu Ile Gly Ser Glu Leu Arg Pro Leu Lys Val Met Ser Ser Val Ser
 60 65 70

acg gcg tgc atg c 318
 Thr Ala Cys Met
 75

<210> 11

<211> 77
<212> PRT
<213> Arabidopsis thaliana

<400> 11

Met Ala Gln Val Ser Arg Ile Cys Asn Gly Val Gln Asn Pro Ser Leu
1 5 10 15

Ile Ser Asn Leu Ser Lys Ser Ser Gln Arg Lys Ser Pro Leu Ser Val
20 25 30

Ser Leu Lys Thr Gln Gln His Pro Arg Ala Tyr Pro Ile Ser Ser Ser
35 40 45

Trp Gly Leu Lys Lys Ser Gly Met Thr Leu Ile Gly Ser Glu Leu Arg
50 55 60

Pro Leu Lys Val Met Ser Ser Val Ser Thr Ala Cys Met
65 70 75

<210> 12
<211> 402
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (87)...(401)

<400> 12
agatctatcg ataagcttga tgtaattgga ggaagatcaa aattttcaat ccccatctt 60

cgattgcttc aattgaagtt tctccg atg gcg caa gtt agc aga atc tgc aat 113
Met Ala Gln Val Ser Arg Ile Cys Asn
1 5

ggt gtg cag aac cca tct ctt atc tcc aat ctc tcg aaa tcc agt caa 161
Gly Val Gln Asn Pro Ser Leu Ile Ser Asn Leu Ser Lys Ser Ser Gln
10 15 20 25

cgc aaa tct ccc tta tcg gtt tct ctg aag acg cag cag cat cca cga 209
Arg Lys Ser Pro Leu Ser Val Ser Leu Lys Thr Gln Gln His Pro Arg
30 35 40

gct tat ccg att tcg tcg tcg tgg gga ttg aag aag agt ggg atg acg 257
Ala Tyr Pro Ile Ser Ser Ser Trp Gly Leu Lys Lys Ser Gly Met Thr
45 50 55

tta att ggc tct gag ctt cgt cct ctt aag gtc atg tct tct gtt tcc 305
Leu Ile Gly Ser Glu Leu Arg Pro Leu Lys Val Met Ser Ser Val Ser
60 65 70

acg gcg gag aaa gcg tcg gag att gta ctt caa ccc att aga gaa atc 353
Thr Ala Glu Lys Ala Ser Glu Ile Val Leu Gln Pro Ile Arg Glu Ile
75 80 85

tcc ggt ctt att aag ttg cct ggc tcc aag tct cta tca aat aga att c 402
Ser Gly Leu Ile Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile
90 95 100 105

<210> 13
<211> 105
<212> PRT
<213> Arabidopsis thaliana

<400> 13

Met Ala Gln Val Ser Arg Ile Cys Asn Gly Val Gln Asn Pro Ser Leu
1 5 10 15

Ile Ser Asn Leu Ser Lys Ser Ser Gln Arg Lys Ser Pro Leu Ser Val
20 25 30

Ser Leu Lys Thr Gln Gln His Pro Arg Ala Tyr Pro Ile Ser Ser Ser
35 40 45

Trp Gly Leu Lys Lys Ser Gly Met Thr Leu Ile Gly Ser Glu Leu Arg
50 55 60

Pro Leu Lys Val Met Ser Ser Val Ser Thr Ala Glu Lys Ala Ser Glu
65 70 75 80

Ile Val Leu Gln Pro Ile Arg Glu Ile Ser Gly Leu Ile Lys Leu Pro
85 90 95

Gly Ser Lys Ser Leu Ser Asn Arg Ile
100 105

<210> 14
<211> 233
<212> DNA
<213> Petunia x hybrida

<220>

<221> CDS
<222> (14)..(232)

<400> 14

agatcttca aga atg gca caa att aac aac atg gct caa ggg ata caa
Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln
1 5 10

49

acc ctt aat ccc aat tcc aat ttc cat aaa ccc caa gtt cct aaa tct
Thr Leu Asn Pro Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser
15 20 25

97

tca agt ttt ctt gtt ttt gga tct aaa aaa ctg aaa aat tca gca aat
Ser Ser Phe Leu Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn
30 35 40

145

tct atg ttg gtt ttg aaa aaa gat tca att ttt atg caa aag ttt tgt
Ser Met Leu Val Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys
45 50 55 60

193

tcc ttt agg att tca gca tca gtg gct aca gcc tgc atg c
Ser Phe Arg Ile Ser Ala Ser Val Ala Thr Ala Cys Met
65 70

233

<210> 15
<211> 73
<212> PRT
<213> Petunia x hybrida

<400> 15

Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro
1 5 10 15

Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu
20 25 30

Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val
35 40 45

Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile
50 55 60

Ser Ala Ser Val Ala Thr Ala Cys Met
65 70

<210> 16
<211> 352

<212> DNA
<213> Petunia x hybrida

<220>

<221> CDS

<222> (49)...(351)

<400> 16

agatctgcta gaaataattt tgtttaactt taagaaggag atatatcc atg gca caa 57
Met Ala Gln
1

att aac aac atg gct caa ggg ata caa acc ctt aat ccc aat tcc aat 105
Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro Asn Ser Asn
5 10 15

ttc cat aaa ccc caa gtt cct aaa tct tca agt ttt ctt gtt ttt gga 153
Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu Val Phe Gly
20 25 30 35

tct aaa aaa ctg aaa aat tca gca aat tct atg ttg gtt ttg aaa aaa 201
Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val Leu Lys Lys
40 45 50

gat tca att ttt atg caa aag ttt tgt tcc ttt agg att tca gca tca 249
Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile Ser Ala Ser
55 60 65

gtg gct aca gca cag aag cct tct gag ata gtg ttg caa ccc att aaa 297
Val Ala Thr Ala Gln Lys Pro Ser Glu Ile Val Leu Gln Pro Ile Lys
70 75 80

gag att tca ggc act gtt aaa ttg cct ggc tct aaa tca tta tct aat 345
Glu Ile Ser Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn
85 90 95

aga att c 352
Arg Ile
100

<210> 17
<211> 101
<212> PRT
<213> Petunia x hybrida

<400> 17

Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro 15
1 5 10 15

Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu
20 25 30

Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val
35 40 45

Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile
50 55 60

Ser Ala Ser Val Ala Thr Ala Gln Lys Pro Ser Glu Ile Val Leu Gln
65 70 75 80

Pro Ile Lys Glu Ile Ser Gly Thr Val Lys Leu Pro Gly Ser Lys Ser
85 90 95

Leu Ser Asn Arg Ile
100

<210> 18
<211> 28
<212> PRT
<213> Agrobacterium sp.

<220>
<221> UNSURE
<222> (1)...(18)
<223> Xaa = Unknown

<400> 18

Xaa His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser Gly
1 5 10 15

Leu Xaa Gly Thr Val Arg Ile Pro Gly Asp Lys Met
20 25

<210> 19
<211> 13
<212> PRT
<213> Agrobacterium sp.

<400> 19

Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val
1 5 10

<210> 20
<211> 15
<212> PRT

<213> Agrobacterium sp.

<400> 20

Ile Thr Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys
1 5 10 15

<210> 21

<211> 17

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic

<400> 21

atgatgagayg artaycc

17

<210> 22

<211> 17

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(17)

<223> R = A or G;

Y = C or T/U;

N = A or C or G or T/U;

H = A or C or T/U

<400> 22

gargaygttna thaacac

17

<210> 23

<211> 17

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic

<220>

<221> misc_feature

<222> (1)..(17)

<223> R = A or G;

Y = C or T/U;

N = A or C or G or T/U;

H = A or C or T/U

<400> 23
gargaygtna thaatac

17

<210> 24
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 24
cgtggataga tcttaggaaga caaccatggc tcacggc

38

<210> 25
<211> 44
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 25
ggatagatta aggaagacgc gcatgttca cggtgcaagc agcc

44

<210> 26
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 26
ggctgcctga ttagctccac aatcgccatc gatgg

35

<210> 27
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 27
cgtcgctcgt cgtgcgtggc cgccctgacg gc

32

<210> 28
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 28

cgggcaaggc catgcaggct atgggcggcc

29

<210> 29
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 29
cgggctgccg cctgactatg ggcctcgatc g

31

<210> 30
<211> 15
<212> PRT
<213> Pseudomonas sp.

<220>
<221> NON_CONS
<222> (1)..(1)
<223> Xaa = unknown

<400> 30

Xaa His Ser Ala Ser Pro Lys Pro Ala Thr Ala Arg Arg Ser Glu
1 5 10 15

<210> 31
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<220>
<221> misc_feature
<222> (1)..(17)
<223> B = C or G or T
S = G or C

Y = C or T

<400> 31
gcgggtbgcsg gyttsgg

17

<210> 32
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<400> 32

Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly Leu
1 5 10 15

<210> 33
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 33

Leu Asp Phe Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr
1 5 10

<210> 34
<211> 26
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 34
cggcaatgcc gccaccggcg cgcgcc

26

<210> 35
<211> 49
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 35

ggacggctgc ttgcaccgtg aagcatgctt aagcttggcg taatcatgg

49

<210> 36
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 36
ggaagacgcc cagaattcac ggtgcaagca gccgg

35

<210> 37
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<220>
<221> NON_CONS
<222> (2)..(2)
<223> Xaa = Gly, Ser, Thr, Cys, Tyr, Asn, Gln, Asp, or Glu

<220>
<221> NON_CONS
<222> (4)..(4)
<223> Xaa = Ser or Thr

<400> 37

Arg Xaa His Xaa Glu
1 5

<210> 38
<211> 4
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic

<220>
<221> NON_CONS
<222> (4)..(4)
<223> Xaa = Ser or Thr

<400> 38

Gly Asp Lys Xaa

1

<210> 39

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic

<220>

<221> NON_CONS

<222> (4)..(4)

<223> Xaa=Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val

<400> 39

Ser Ala Gln Xaa Lys

1

5

<210> 40

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic

<220>

<221> NON_CONS

<222> (2)..(2)

<223> Xaa=Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val

<400> 40

Asn Xaa Thr Arg

1

<210> 41

<211> 1287

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(1287)

<400> 41
 atg aaa cga gat aag gtg cag acc tta cat gga gaa ata cat att ccc 48
 Met Lys Arg Asp Lys Val Gln Thr Leu His Gly Glu Ile His Ile Pro
 1 5 10 15

 ggt gat aaa tcc att tct cac cgc tct gtt atg ttt ggc gcg cta gcg 96
 Gly Asp Lys Ser Ile Ser His Arg Ser Val Met Phe Gly Ala Leu Ala
 20 25 30

 gca ggc aca aca aca gtt aaa aac ttt ctg ccg gga gca gat tgt ctg 144
 Ala Gly Thr Thr Val Lys Asn Phe Leu Pro Gly Ala Asp Cys Leu
 35 40 45

 agc acg atc gat tgc ttt aga aaa atg ggt gtt cac att gag caa agc 192
 Ser Thr Ile Asp Cys Phe Arg Lys Met Gly Val His Ile Glu Gln Ser
 50 55 60

 agc agc gat gtc gtg att cac gga aaa gga atc gat gcc ctg aaa gag 240
 Ser Ser Asp Val Val Ile His Gly Lys Gly Ile Asp Ala Leu Lys Glu
 65 70 75 80

 cca gaa agc ctt tta gat gtc gga aat tca ggt aca acg att cgc ctg 288
 Pro Glu Ser Leu Leu Asp Val Gly Asn Ser Gly Thr Thr Ile Arg Leu
 85 90 95

 atg ctc gga ata ttg gcg ggc cgt cct ttt tac agc gcg gta gcc gga 336
 Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly
 100 105 110

 gat gag agc att gcg aaa cgc cca atg aag cgt gtg act gag cct ttg 384
 Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu
 115 120 125

 aaa aaa atg ggg gct aaa atc gac ggc aga gcc ggc gga gag ttt aca 432
 Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Glu Phe Thr
 130 135 140

 ccg ctg tca gtg agc ggc gct tca tta aaa gga att gat tat gta tca 480
 Pro Leu Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser
 145 150 155 160

 cct gtt gca agc gcg caa att aaa tct gct gtt ttg ctg gcc gga tta 528
 Pro Val Ala Ser Ala Gln Ile Lys Ser Ala Val Leu Leu Ala Gly Leu
 165 170 175

 cag gct gag ggc aca aca act gta aca gag ccc cat aaa tct cg gac 576
 Gln Ala Glu Gly Thr Thr Val Thr Glu Pro His Lys Ser Arg Asp
 180 185 190

 cac act gag cgg atg ctt tct gct ttt ggc gtt aag ctt tct gaa gat 624
 His Thr Glu Arg Met Leu Ser Ala Phe Gly Val Lys Leu Ser Glu Asp
 195 200 205

caa acg agt gtt tcc att gct ggt ggc cag aaa ctg aca gct gct gat		672	
Gln Thr Ser Val Ser Ile Ala Gly Gly Gln Lys Leu Thr Ala Ala Asp			
210	215	220	
att ttt gtt cct gga gac att tct tca gcc gcg ttt ttc ctt gct gct		720	
Ile Phe Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Phe Leu Ala Ala			
225	230	235	240
ggc gcg atg gtt cca aac agc aga att gta ttg aaa aac gta ggt tta		768	
Gly Ala Met Val Pro Asn Ser Arg Ile Val Leu Lys Asn Val Gly Leu			
245	250	255	
aat ccg act cgg aca ggt att att gat gtc ctt caa aac atg ggg gca		816	
Asn Pro Thr Arg Thr Gly Ile Ile Asp Val Leu Gln Asn Met Gly Ala			
260	265	270	
aaa ctt gaa atc aaa cca tct gct gat agc ggt gca gag cct tat gga		864	
Lys Leu Glu Ile Lys Pro Ser Ala Asp Ser Gly Ala Glu Pro Tyr Gly			
275	280	285	
gat ttg att ata gaa acg tca tct cta aag gca gtt gaa atc gga gga		912	
Asp Leu Ile Ile Glu Thr Ser Ser Leu Lys Ala Val Glu Ile Gly Gly			
290	295	300	
gat atc att ccg cgt tta att gat gag atc cct atc atc gcg ctt ctt		960	
Asp Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Ile Ala Leu Leu			
305	310	315	320
gcg act cag gcg gaa gga acc acc gtt att aag gac gcg gca gag cta		1008	
Ala Thr Gln Ala Glu Gly Thr Thr Val Ile Lys Asp Ala Ala Glu Leu			
325	330	335	
aaa gtg aaa gaa aca aac cgt att gat act gtt gtt tct gag ctt cgc		1056	
Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Val Val Ser Glu Leu Arg			
340	345	350	
aag ctg ggt gct gaa att gaa ccg aca gca gat gga atg aag gtt tat		1104	
Lys Leu Gly Ala Glu Ile Glu Pro Thr Ala Asp Gly Met Lys Val Tyr			
355	360	365	
ggc aaa caa acg ttg aaa ggc ggc gct gca gtg tcc agc cac gga gat		1152	
Gly Lys Gln Thr Leu Lys Gly Gly Ala Ala Val Ser Ser His Gly Asp			
370	375	380	
cat cga atc gga atg atg ctt ggt att gct tcc tgt ata acg gag gag		1200	
His Arg Ile Gly Met Met Leu Gly Ile Ala Ser Cys Ile Thr Glu Glu			
385	390	395	400
ccg att gaa atc gag cac acg gat gcc att cac gtt tct tat cca acc		1248	
Pro Ile Glu Ile Glu His Thr Asp Ala Ile His Val Ser Tyr Pro Thr			
405	410	415	
ttc ttc gag cat tta aat aag ctt tcg aaa aaa tcc tga		1287	
Phe Phe His Leu Asn Lys Leu Ser Lys Lys Ser			

<210> 42
 <211> 428
 <212> PRT
 <213> *Bacillus subtilis*

<400> 42

Met Lys Arg Asp Lys Val Gln Thr Leu His Gly Glu Ile His Ile Pro
 1 5 10 15

Gly Asp Lys Ser Ile Ser His Arg Ser Val Met Phe Gly Ala Leu Ala
 20 25 30

Ala Gly Thr Thr Val Lys Asn Phe Leu Pro Gly Ala Asp Cys Leu
 35 40 45

Ser Thr Ile Asp Cys Phe Arg Lys Met Gly Val His Ile Glu Gln Ser
 50 55 60

Ser Ser Asp Val Val Ile His Gly Lys Gly Ile Asp Ala Leu Lys Glu
 65 70 75 80

Pro Glu Ser Leu Leu Asp Val Gly Asn Ser Gly Thr Thr Ile Arg Leu
 85 90 95

Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly
 100 105 110

Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu
 115 120 125

Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Gly Glu Phe Thr
 130 135 140

Pro Leu Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser
 145 150 155 160

Pro Val Ala Ser Ala Gln Ile Lys Ser Ala Val Leu Leu Ala Gly Leu
 165 170 175

Gln Ala Glu Gly Thr Thr Val Thr Glu Pro His Lys Ser Arg Asp
180 185 190

His Thr Glu Arg Met Leu Ser Ala Phe Gly Val Lys Leu Ser Glu Asp
195 200 205

Gln Thr Ser Val Ser Ile Ala Gly Gly Gln Lys Leu Thr Ala Ala Asp
210 215 220

Ile Phe Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Phe Leu Ala Ala
225 230 235 240

Gly Ala Met Val Pro Asn Ser Arg Ile Val Leu Lys Asn Val Gly Leu
245 250 255

Asn Pro Thr Arg Thr Gly Ile Ile Asp Val Leu Gln Asn Met Gly Ala
260 265 270

Lys Leu Glu Ile Lys Pro Ser Ala Asp Ser Gly Ala Glu Pro Tyr Gly
275 280 285

Asp Leu Ile Ile Glu Thr Ser Ser Leu Lys Ala Val Glu Ile Gly Gly
290 295 300

Asp Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Ile Ala Leu Leu
305 310 315 320

Ala Thr Gln Ala Glu Gly Thr Thr Val Ile Lys Asp Ala Ala Glu Leu
325 330 335

Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Val Val Ser Glu Leu Arg
340 345 350

Lys Leu Gly Ala Glu Ile Glu Pro Thr Ala Asp Gly Met Lys Val Tyr
355 360 365

Gly Lys Gln Thr Leu Lys Gly Gly Ala Ala Val Ser Ser His Gly Asp
370 375 380

His Arg Ile Gly Met Met Leu Gly Ile Ala Ser Cys Ile Thr Glu Glu
385 390 395 400

Pro Ile Glu Ile Glu His Thr Asp Ala Ile His Val Ser Tyr Pro Thr
405 410 415

Phe Phe Glu His Leu Asn Lys Leu Ser Lys Lys Ser
420 425

<210> 43
<211> 1293
<212> DNA
<213> *Staphylococcus aureus*

<220>
<221> CDS
<222> (1)..(1293)

<400> 43
atg gta aat gaa caa atc att gat att tca ggt ccg tta aag ggc gaa 48
Met Val Asn Glu Gln Ile Ile Asp Ile Ser Gly Pro Leu Lys Gly Glu
1 5 10 15

ata gaa gtg ccg ggc gat aag tca atg aca cac cgt gca atc atg ttg 96
Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu
20 25 30

gcg tcg cta gct gaa ggt gta tct act ata tat aag cca cta ctt ggc 144
Ala Ser Leu Ala Glu Gly Val Ser Thr Ile Tyr Lys Pro Leu Leu Gly
35 40 45

gaa gat tgt cgt acg atg gac att ttc cga cac tta ggt gta gaa 192
Glu Asp Cys Arg Arg Thr Met Asp Ile Phe Arg His Leu Gly Val Glu
50 55 60

atc aaa gaa gat gat gaa aaa tta gtt gtg act tcc cca gga tat caa 240
Ile Lys Glu Asp Asp Glu Lys Leu Val Val Thr Ser Pro Gly Tyr Gln
65 70 75 80

gtt aac acg cca cat caa gta ttg tat aca ggt aat tct ggt acg aca 288
Val Asn Thr Pro His Gln Val Leu Tyr Thr Gly Asn Ser Gly Thr Thr
85 90 95

aca cga tta ttg gca ggt ttg tta agt ggt tta ggt aat gaa agt gtt 336
Thr Arg Leu Leu Ala Gly Leu Leu Ser Gly Leu Gly Asn Glu Ser Val
100 105 110

ttg tct ggc gat gtt tca att ggt aaa agg cca atg gat cgt gtc ttg 384
Leu Ser Gly Asp Val Ser Ile Gly Lys Arg Pro Met Asp Arg Val Leu
115 120 125

aga cca ttg aaa ctt atg gat gcg aat att gaa ggt att gaa gat aat 432
Arg Pro Leu Lys Leu Met Asp Ala Asn Ile Glu Gly Ile Glu Asp Asn

130	135	140	
tat aca cca tta att att aag cca tct gtc ata aaa ggt ata aat tat Tyr Thr Pro Leu Ile Ile Lys Pro Ser Val Ile Lys Gly Ile Asn Tyr			480
145	150	155	160
caa atg gaa gtt gca agt gca caa gta aaa agt gcc att tta ttt gca Gln Met Glu Val Ala Ser Ala Gln Val Lys Ser Ala Ile Leu Phe Ala			528
165	170		175
agt ttg ttt tct aag gaa ccg acc atc att aaa gaa tta gat gta agt Ser Leu Phe Ser Lys Glu Pro Thr Ile Ile Lys Glu Leu Asp Val Ser			576
180	185		190
cga aat cat act gag acg atg ttc aaa cat ttt aat att cca att gaa Arg Asn His Thr Glu Thr Met Phe Lys His Phe Asn Ile Pro Ile Glu			624
195	200		205
gca gaa ggg tta tca att aat aca acc cct gaa gca att cga tac att Ala Glu Gly Leu Ser Ile Asn Thr Thr Pro Glu Ala Ile Arg Tyr Ile			672
210	215		220
aaa cct gca gat ttt cat gtt cct ggc gat att tca tct gca gcg ttc Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe			720
225	230		235
ttt att gtt gca gca ctt atc aca cca gga agt gat gta aca att cat Phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His			768
245	250		255
aat gtt gga atc aat caa aca cgt tca ggt att att gat att gtt gaa Asn Val Gly Ile Asn Gln Thr Arg Ser Gly Ile Ile Asp Ile Val Glu			816
260	265		270
aaa atg ggc ggt aat atc caa ctt ttc aat caa aca act ggt gct gaa Lys Met Gly Gly Asn Ile Gln Leu Phe Asn Gln Thr Thr Gly Ala Glu			864
275	280		285
cct act gct tct att cgt att caa tac aca cca atg ctt caa cca ata Pro Thr Ala Ser Ile Arg Ile Gln Tyr Thr Pro Met Leu Gln Pro Ile			912
290	295		300
aca atc gaa gga gaa tta gtt cca aaa gca att gat gaa ctg cct gta Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val			960
305	310		315
ata gca tta ctt tgt aca caa gca gtt ggc acg agt aca att aaa gat Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp			1008
325	330		335
gcc gag gaa tta aaa gta aaa gaa aca aat aga att gat aca acg gct Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala			1056
340	345		350

gat atg tta aac ttg tta ggg ttt gaa tta caa cca act aat gat gga 1104
Asp Met Leu Asn Leu Leu Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly
355 360 365

ttg att att cat ccg tca gaa ttt aaa aca aat gca aca gat att tta 1152
Leu Ile Ile His Pro Ser Glu Phe Lys Thr Asn Ala Thr Asp Ile Leu
370 375 380

act gat cat cga ata gga atg atg ctt gca gtt gct tgt gta ctt tca 1200
Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser
385 390 395 400

agc gag cct gtc aaa atc aaa caa ttt gat gct gta aat gta tca ttt 1248
Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe
405 410 415

cca gga ttt tta cca aaa cta aag ctt tta caa aat gag gga taa 1293
Pro Gly Phe Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly
420 425 430

<210> 44
<211> 430
<212> PRT
<213> Staphylococcus aureus

<400> 44

Met Val Asn Glu Gln Ile Ile Asp Ile Ser Gly Pro Leu Lys Gly Glu
1 5 10 15

Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu
20 25 30

Ala Ser Leu Ala Glu Gly Val Ser Thr Ile Tyr Lys Pro Leu Leu Gly
35 40 45

Glu Asp Cys Arg Arg Thr Met Asp Ile Phe Arg His Leu Gly Val Glu
50 55 60

Ile Lys Glu Asp Asp Glu Lys Leu Val Val Thr Ser Pro Gly Tyr Gln
65 70 75 80

Val Asn Thr Pro His Gln Val Leu Tyr Thr Gly Asn Ser Gly Thr Thr
85 90 95

Thr Arg Leu Leu Ala Gly Leu Leu Ser Gly Leu Gly Asn Glu Ser Val
100 105 110

Leu Ser Gly Asp Val Ser Ile Gly Lys Arg Pro Met Asp Arg Val Leu
115 120 125

Arg Pro Leu Lys Leu Met Asp Ala Asn Ile Glu Gly Ile Glu Asp Asn
130 135 140

Tyr Thr Pro Leu Ile Ile Lys Pro Ser Val Ile Lys Gly Ile Asn Tyr
145 150 155 160

Gln Met Glu Val Ala Ser Ala Gln Val Lys Ser Ala Ile Leu Phe Ala
165 170 175

Ser Leu Phe Ser Lys Glu Pro Thr Ile Ile Lys Glu Leu Asp Val Ser
180 185 190

Arg Asn His Thr Glu Thr Met Phe Lys His Phe Asn Ile Pro Ile Glu
195 200 205

Ala Glu Gly Leu Ser Ile Asn Thr Thr Pro Glu Ala Ile Arg Tyr Ile
210 215 220

Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe
225 230 235 240

Phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His
245 250 255

Asn Val Gly Ile Asn Gln Thr Arg Ser Gly Ile Ile Asp Ile Val Glu
260 265 270

Lys Met Gly Gly Asn Ile Gln Leu Phe Asn Gln Thr Thr Gly Ala Glu
275 280 285

Pro Thr Ala Ser Ile Arg Ile Gln Tyr Thr Pro Met Leu Gln Pro Ile
290 295 300

Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val
305 310 315 320

Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp
325 330 335

Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala
340 345 350

Asp Met Leu Asn Leu Leu Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly
355 360 365

Leu Ile Ile His Pro Ser Glu Phe Lys Thr Asn Ala Thr Asp Ile Leu
370 375 380

Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser
385 390 395 400

Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe
405 410 415

Pro Gly Phe Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly
420 425 430

<210> 45
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 45
ggaacatatg aaacgagata aggtgcag

28

<210> 46
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 46
ggaattcaaa cttcaggatc ttgagataga aaatg

35

<210> 47
<211> 28

<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 47
ggggccatgg taaatgaaca aatcattg

28

<210> 48
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> Oligonucleotide

<400> 48
gggggagctc attatccctc attttgtaaa agc

33

<210> 49
<211> 480
<212> PRT
<213> Saccharomyces cerevisiae

<400> 49

Leu Thr Asp Glu Thr Leu Val Tyr Pro Phe Lys Asp Ile Pro Ala Asp
1 5 10 15

Gln Gln Lys Val Val Ile Pro Pro Gly Ser Lys Ser Ile Ser Asn Arg
20 25 30

Ala Leu Ile Leu Ala Ala Leu Gly Glu Gly Gln Cys Lys Ile Lys Asn
35 40 45

Leu Leu His Ser Asp Asp Thr Lys His Met Leu Thr Ala Val His Glu
50 55 60

Leu Lys Gly Ala Thr Ile Ser Trp Glu Asp Asn Gly Glu Thr Val Val
65 70 75 80

Val Glu Gly His Gly Ser Thr Leu Ser Ala Cys Ala Asp Pro Leu
85 90 95

Tyr Leu Gly Asn Ala Gly Thr Ala Ser Arg Phe Leu Thr Ser Leu Ala
100 105 110

Ala Leu Val Asn Ser Thr Ser Ser Gln Lys Tyr Ile Val Leu Thr Gly
115 120 125

Asn Ala Arg Met Gln Gln Arg Pro Ile Ala Pro Leu Val Asp Ser Leu

130 135 140

Arg Ala Asn Gly Thr Lys Ile Glu Tyr Leu Asn Asn Glu Gly Ser Leu
145 150 155 160

Pro Ile Lys Val Tyr Thr Asp Ser Val Phe Lys Gly Gly Arg Ile Glu
165 170 175

Leu Ala Ala Thr Val Ser Ser Gln Tyr Val Ser Ser Ile Leu Met Cys
180 185 190

Ala Pro Tyr Ala Glu Glu Pro Val Thr Leu Ala Leu Val Gly Gly Lys
195 200 205

Pro Ile Ser Lys Leu Tyr Val Asp Met Thr Ile Lys Met Met Glu Lys
210 215 220

Phe Gly Ile Asn Val Glu Thr Ser Thr Thr Glu Pro Tyr Thr Tyr Tyr
225 230 235 240

Ile Pro Lys Gly His Tyr Ile Asn Pro Ser Glu Tyr Val Ile Glu Ser
245 250 255

Asp Ala Ser Ser Ala Thr Tyr Pro Leu Ala Phe Ala Ala Met Thr Gly
260 265 270

Thr Thr Val Thr Val Pro Asn Ile Gly Phe Glu Ser Leu Gln Gly Asp
275 280 285

Ala Arg Phe Ala Arg Asp Val Leu Lys Pro Met Gly Cys Lys Ile Thr
290 295 300

Gln Thr Ala Thr Ser Thr Val Ser Gly Pro Pro Val Gly Thr Leu
305 310 315 320

Lys Pro Leu Lys His Val Asp Met Glu Pro Met Thr Asp Ala Phe Leu
325 330 335

Thr Ala Cys Val Val Ala Ala Ile Ser His Asp Ser Asp Pro Asn Ser
340 345 350

Ala Asn Thr Thr Thr Ile Glu Gly Ile Ala Asn Gln Arg Val Lys Glu
355 360 365

Cys Asn Arg Ile Leu Ala Met Ala Thr Glu Leu Ala Lys Phe Gly Val
370 375 380

Lys Thr Thr Glu Leu Pro Asp Gly Ile Gln Val His Gly Leu Asn Ser
385 390 395 400

Ile Lys Asp Leu Lys Val Pro Ser Asp Ser Ser Gly Pro Val Gly Val
405 410 415

Cys Thr Tyr Asp Asp His Arg Val Ala Met Ser Phe Ser Leu Leu Ala

420

425

430

Gly Met Val Asn Ser Gln Asn Glu Arg Asp Glu Val Ala Asn Pro Val
 435 440 445

Arg Ile Leu Glu Arg His Cys Thr Gly Lys Thr Trp Pro Gly Trp Trp
 450 455 460

Asp Val Leu His Ser Glu Leu Gly Ala Lys Leu Asp Gly Ala Glu Pro
 465 470 475 480

<210> 50

<211> 460

<212> PRT

<213> Aspergillus ridulaus

<400> 50

Leu Ala Pro Ser Ile Glu Val His Pro Gly Val Ala His Ser Ser Asn
 1 5 10 15

Val Ile Cys Ala Pro Pro Gly Ser Lys Ser Ile Ser Asn Arg Ala Leu
 20 25 30

Val Leu Ala Ala Leu Gly Ser Gly Thr Cys Arg Ile Lys Asn Leu Leu
 35 40 45

His Ser Asp Asp Thr Glu Val Met Leu Asn Ala Leu Glu Arg Leu Gly
 50 55 60

Ala Ala Thr Phe Ser Trp Glu Glu Gly Glu Val Leu Val Val Asn
 65 70 75 80

Gly Lys Gly Gly Asn Leu Gln Ala Ser Ser Ser Pro Leu Tyr Leu Gly
 85 90 95

Asn Ala Gly Thr Ala Ser Arg Phe Leu Thr Thr Val Ala Thr Leu Ala
 100 105 110

Asn Ser Ser Thr Val Asp Ser Ser Val Leu Thr Gly Asn Asn Arg Met
 115 120 125

Lys Gln Arg Pro Ile Gly Asp Leu Val Asp Ala Leu Thr Ala Asn Val
 130 135 140

Leu Pro Leu Asn Thr Ser Lys Gly Arg Ala Ser Leu Pro Leu Lys Ile
 145 150 155 160

Ala Ala Ser Gly Gly Phe Ala Gly Asn Ile Asn Leu Ala Ala Lys
 165 170 175

Val Ser Ser Gln Tyr Val Ser Ser Leu Leu Met Cys Ala Pro Tyr Ala
 180 185 190

Lys Glu Pro Val Thr Leu Arg Leu Val Gly Gly Lys Pro Ile Ser Gln
195 200 205

Pro Tyr Ile Asp Met Thr Thr Ala Met Met Arg Ser Phe Gly Ile Asp
210 215 220

Val Gln Lys Ser Thr Thr Glu Glu His Thr Tyr His Ile Pro Gln Gly
225 230 235 240

Arg Tyr Val Asn Pro Ala Glu Tyr Val Ile Glu Ser Asp Ala Ser Cys
245 250 255

Ala Thr Tyr Pro Leu Ala Val Ala Val Thr Gly Thr Thr Cys Thr
260 265 270

Val Pro Asn Ile Gly Ser Ala Ser Leu Gln Gly Asp Ala Arg Phe Ala
275 280 285

Val Glu Val Leu Arg Pro Met Gly Cys Thr Val Glu Gln Thr Glu Thr
290 295 300

Ser Thr Thr Val Thr Gly Pro Ser Asp Gly Ile Leu Arg Ala Thr Ser
305 310 315 320

Lys Arg Gly Tyr Gly Thr Asn Asp Arg Cys Val Pro Arg Cys Phe Arg
325 330 335

Thr Gly Ser His Arg Pro Met Glu Lys Ser Gln Thr Thr Pro Pro Val
340 345 350

Ser Ser Gly Ile Ala Asn Gln Arg Val Lys Glu Cys Asn Arg Ile Lys
355 360 365

Ala Met Lys Asp Glu Leu Ala Lys Phe Gly Val Ile Cys Arg Glu His
370 375 380

Asp Asp Gly Leu Glu Ile Asp Gly Ile Asp Arg Ser Asn Leu Arg Gln
385 390 395 400

Pro Val Gly Gly Val Phe Cys Tyr Asp Asp His Arg Val Ala Phe Ser
405 410 415

Phe Ser Val Leu Ser Leu Val Thr Pro Gln Pro Thr Leu Ile Leu Glu
420 425 430

Lys Glu Cys Val Gly Lys Thr Trp Pro Gly Trp Trp Asp Thr Leu Arg
435 440 445

Gln Leu Phe Lys Val Lys Leu Glu Gly Lys Glu Leu
450 455 460

<210> 51
<211> 444
<212> PRT

<213> Brassica napus

<400> 51

Lys Ala Ser Glu Ile Val Leu Gln Pro Ile Arg Glu Ile Ser Gly Leu
1 5 10 15

Ile Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
20 25 30

Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn Ser
35 40 45

Asp Asp Ile Asn Tyr Met Leu Asp Ala Leu Lys Lys Leu Gly Leu Asn
50 55 60

Val Glu Arg Asp Ser Val Asn Asn Arg Ala Val Val Glu Gly Cys Gly
65 70 75 80

Gly Ile Phe Pro Ala Ser Leu Asp Ser Lys Ser Asp Ile Glu Leu Tyr
85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110

Ala Ala Gly Gly Asn Ala Ser Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
130 135 140

Ala Asp Val Glu Cys Thr Leu Gly Thr Asn Cys Pro Pro Val Arg Val
145 150 155 160

Asn Ala Asn Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ala Ala Pro Leu Ala
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Val Pro
195 200 205

Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Val Ser Ala
210 215 220

Glu His Ser Asp Ser Trp Asp Arg Phe Phe Val Lys Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Gly Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Glu Thr Val Thr Val
260 265 270

Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Lys Met Gly Cys Lys Val Ser Trp Thr Glu Asn Ser Val
290 295 300

Thr Val Thr Gly Pro Ser Arg Asp Ala Phe Gly Met Arg His Leu Arg
305 310 315 320

Ala Val Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Thr Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
355 360 365

Glu Leu Arg Lys Leu Gly Ala Thr Val Glu Glu Gly Ser Asp Tyr Cys
370 375 380

Val Ile Thr Pro Pro Ala Lys Val Lys Pro Ala Glu Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
405 410 415

Val Pro Val Thr Ile Lys Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430

Asp Tyr Phe Gln Val Leu Glu Ser Ile Thr Lys His
435 440

<210> 52
<211> 444
<212> PRT
<213> Arabidopsis thaliana

<400> 52

Lys Ala Ser Glu Ile Val Leu Gln Pro Ile Arg Glu Ile Ser Gly Leu
1 5 10 15

Ile Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
20 25 30

Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn Ser
35 40 45

Asp Asp Ile Asn Tyr Met Leu Asp Ala Leu Lys Arg Leu Gly Leu Asn
50 55 60

Val Glu Thr Asp Ser Glu Asn Asn Arg Ala Val Val Glu Gly Cys Gly

65

70

75

80

Gly Ile Phe Pro Ala Ser Ile Asp Ser Lys Ser Asp Ile Glu Leu Tyr
85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110

Ala Ala Gly Gly Asn Ala Ser Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
130 135 140

Ala Asp Val Glu Cys Thr Leu Gly Thr Asn Cys Pro Pro Val Arg Val
145 150 155 160

Asn Ala Asn Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ser Ala Pro Leu Ala
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Val Asp Lys Leu Ile Ser Val Pro
195 200 205

Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Val Ser Val
210 215 220

Glu His Ser Asp Ser Trp Asp Arg Phe Phe Val Lys Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Gly Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Cys Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Glu Thr Val Thr Val
260 265 270

Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Lys Met Gly Cys Lys Val Ser Trp Thr Glu Asn Ser Val
290 295 300

Thr Val Thr Gly Pro Pro Arg Asp Ala Phe Gly Met Arg His Leu Arg
305 310 315 320

Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Thr Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr

355

360

365

Glu Leu Arg Lys Leu Gly Ala Thr Val Glu Glu Gly Ser Asp Tyr Cys
370 375 380

Val Ile Thr Pro Pro Lys Lys Val Lys Thr Ala Glu Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
405 410 415

Val Pro Ile Thr Ile Asn Asp Ser Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430

Asp Tyr Phe Gln Val Leu Glu Arg Ile Thr Lys His
435 440

<210> 53

<211> 444

<212> PRT

<213> Nicotiana tabacum

<400> 53

Lys Pro Asn Glu Ile Val Leu Gln Pro Ile Lys Asp Ile Ser Gly Thr
1 5 10 15

Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
20 25 30

Ala Ala Leu Ser Lys Gly Arg Thr Val Val Asp Asn Leu Leu Ser Ser
35 40 45

Asp Asp Ile His Tyr Met Leu Gly Ala Leu Lys Thr Leu Gly Leu His
50 55 60

Val Glu Asp Asp Asn Glu Asn Gln Arg Ala Ile Val Glu Gly Cys Gly
65 70 75 80

Gly Gln Phe Pro Val Gly Lys Ser Glu Glu Ile Gln Leu Phe
85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110

Val Ala Gly Gly His Ser Arg Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Asp Gly Leu Lys Gln Leu Gly
130 135 140

Ala Glu Val Asp Cys Phe Leu Gly Thr Asn Cys Pro Pro Val Arg Ile
145 150 155 160

Val Ser Lys Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ala Ala Pro Leu Ala
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Val Pro
195 200 205

Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Val Ser Val
210 215 220

Glu His Thr Ser Ser Trp Asp Lys Phe Leu Val Arg Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Gly Lys Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Val Thr Gly Gly Thr Val Thr Val
260 265 270

Glu Gly Cys Gly Thr Ser Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Lys Met Gly Ala Glu Val Thr Trp Thr Glu Asn Ser Val
290 295 300

Thr Val Lys Gly Pro Pro Arg Asn Ser Ser Gly Met Lys His Leu Arg
305 310 315 320

Ala Val Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
355 360 365

Glu Leu Arg Lys Leu Gly Ala Thr Val Val Glu Gly Ser Asp Tyr Cys
370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Glu Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
405 410 415

Val Pro Val Thr Ile Lys Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430

Asn Tyr Phe Asp Val Leu Gln Gln Tyr Ser Lys His
435 440

<210> 54
<211> 444
<212> PRT
<213> Lycopersicon esculentum

<220>
<221> UNSURE
<222> (1)..(444)
<223> Xaa = any

<400> 54

Lys Pro His Glu Ile Val Leu Xaa Pro Ile Lys Asp Ile Ser Gly Thr
1 5 10 15

Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu Leu
20 25 30

Ala Ala Leu Ser Glu Gly Arg Thr Val Val Asp Asn Leu Leu Ser Ser
35 40 45

Asp Asp Ile His Tyr Met Leu Gly Ala Leu Lys Thr Leu Gly Leu His
50 55 60

Val Glu Asp Asp Asn Glu Asn Gln Arg Ala Ile Val Glu Gly Cys Gly
65 70 75 80

Gly Gln Phe Pro Val Gly Lys Ser Glu Glu Glu Ile Gln Leu Phe
85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110

Val Ala Gly Gly His Ser Arg Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Asp Gly Leu Lys Gln Leu Gly
130 135 140

Ala Glu Val Asp Cys Ser Leu Gly Thr Asn Cys Pro Pro Val Arg Ile
145 150 155 160

Val Ser Lys Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ala Ala Pro Leu Ala
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Val Pro
195 200 205

Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Val Phe Val
210 215 220

Glu His Ser Ser Gly Trp Asp Arg Phe Leu Val Lys Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Gly Lys Ala Phe Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Val Thr Gly Gly Thr Val Thr Val
260 265 270

Glu Gly Cys Gly Thr Ser Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Lys Met Gly Ala Glu Val Thr Trp Thr Glu Asn Ser Val
290 295 300

Thr Val Lys Gly Pro Pro Arg Asn Ser Ser Gly Met Lys His Leu Arg
305 310 315 320

Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Thr Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr
355 360 365

Glu Leu Arg Lys Leu Gly Ala Thr Val Val Glu Gly Ser Asp Tyr Cys
370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Glu Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp
405 410 415

Val Pro Val Thr Ile Lys Asn Pro Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430

Asp Tyr Phe Glu Val Leu Gln Lys Tyr Ser Lys His
435 440

<210> 55
<211> 444
<212> PRT
<213> Petunia x hybrida

<400> 55

Lys Pro Ser Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly Thr
1 5 10 15

Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu

20

25

30

Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Ser Ser
35 40 45

Asp Asp Ile His Tyr Met Leu Gly Ala Leu Lys Thr Leu Gly Leu His
50 55 60

Val Glu Glu Asp Ser Ala Asn Gln Arg Ala Val Val Glu Gly Cys Gly
65 70 75 80

Gly Leu Phe Pro Val Gly Lys Glu Ser Lys Glu Glu Ile Gln Leu Phe
85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110

Val Ala Gly Gly Asn Ser Arg Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Ser Asp Leu Val Asp Gly Leu Lys Gln Leu Gly
130 135 140

Ala Glu Val Asp Cys Phe Leu Gly Thr Lys Cys Pro Pro Val Arg Ile
145 150 155 160

Val Ser Lys Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Thr Ala Leu Leu Met Ala Ala Pro Leu Ala
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Val Pro
195 200 205

Tyr Val Glu Met Thr Leu Lys Leu Met Glu Arg Phe Gly Ile Ser Val
210 215 220

Glu His Ser Ser Ser Trp Asp Arg Phe Phe Val Arg Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Gly Lys Ala Phe Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Val Thr Gly Gly Thr Ile Thr Val
260 265 270

Glu Gly Cys Gly Thr Asn Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Lys Met Gly Ala Glu Val Thr Trp Thr Glu Asn Ser Val
290 295 300

Thr Val Lys Gly Pro Pro Arg Ser Ser Ser Gly Arg Lys His Leu Arg

305	310	315	320
Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu			
325	330	335	
Ala Val Val Ala Leu Tyr Ala Asp Gly Pro Thr Ala Ile Arg Asp Val			
340	345	350	
Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Ile Ala Ile Cys Thr			
355	360	365	
Glu Leu Arg Lys Leu Gly Ala Thr Val Glu Glu Gly Pro Asp Tyr Cys			
370	375	380	
Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Asp Ile Asp Thr Tyr			
385	390	395	400
Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp			
405	410	415	
Val Pro Val Thr Ile Asn Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro			
420	425	430	
Asn Tyr Phe Asp Val Leu Gln Gln Tyr Ser Lys His			
435	440		
<210> 56			
<211> 444			
<212> PRT			
<213> Zea mays			
<400> 56			
Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly			
1	5	10	15
Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu			
20	25	30	
Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn			
35	40	45	
Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu			
50	55	60	
Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys			
65	70	75	80
Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe			
85	90	95	
Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr			
100	105	110	

Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
130 135 140

Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
145 150 155 160

Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Pro
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
195 200 205

Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
210 215 220

Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
260 265 270

Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285

Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
290 295 300

Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
305 310 315 320

Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335

Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
355 360 365

Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
405 410 415

Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430

Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
435 440

<210> 57

<211> 427

<212> PRT

<213> *Salmonella gallinarum*

<400> 57

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
1 5 10 15

Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala
20 25 30

Ala Leu Ala Cys Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
35 40 45

Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Ile Asn Tyr
50 55 60

Thr Leu Ser Ala Asp Arg Thr Arg Cys Asp Ile Thr Gly Asn Gly Gly
65 70 75 80

Pro Leu Arg Ala Pro Gly Ala Leu Glu Leu Phe Leu Gly Asn Ala Gly
85 90 95

Thr Ala Met Arg Pro Leu Ala Ala Leu Cys Leu Gly Gln Asn Glu.
100 105 110

Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
115 120 125

Leu Val Asp Ser Leu Arg Gln Gly Gly Ala Asn Ile Asp Tyr Leu Glu
130 135 140

Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Ile Gly Gly
145 150 155 160

Asp Ile Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
165 170 175

Leu Met Thr Ala Pro Leu Ala Pro Lys Asp Thr Ile Ile Arg Val Lys
180 185 190

Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met
195 200 205

Lys Thr Phe Gly Val Glu Ile Ala Asn His His Tyr Gln Gln Phe Val
210 215 220

Val Lys Gly Gly Gln Gln Tyr His Ser Pro Gly Arg Tyr Leu Val Glu
225 230 235 240

Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Ala Ile Lys
245 250 255

Gly Gly Thr Val Lys Val Thr Gly Ile Gly Arg Lys Ser Met Gln Gly
260 265 270

Asp Ile Arg Phe Ala Asp Val Leu Glu Lys Met Gly Ala Thr Ile Thr
275 280 285

Trp Gly Asp Asp Phe Ile Ala Cys Thr Arg Gly Glu Leu His Ala Ile
290 295 300

Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
305 310 315 320

Thr Ala Leu Phe Ala Lys Gly Thr Thr Leu Arg Asn Ile Tyr Asn
325 330 335

Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
340 345 350

Arg Lys Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile
355 360 365

Thr Pro Pro Ala Lys Leu Gln His Ala Asp Ile Gly Thr Tyr Asn Asp
370 375 380

His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
385 390 395 400

Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
405 410 415

Phe Glu Gln Leu Ala Arg Met Ser Thr Pro Ala
420 425

<210> 58

<211> 427

<212> PRT

<213> *Salmonella typhimurium*

<400> 58

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
1 5 10 15

Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala

20

25

30

Ala Leu Ala Cys Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
 35 40 45

Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Ile Asn Tyr
 50 55 60

Thr Leu Ser Ala Asp Arg Thr Arg Cys Asp Ile Thr Gly Asn Gly Gly
 65 70 75 80

Pro Leu Arg Ala Ser Gly Thr Leu Glu Leu Phe Leu Gly Asn Ala Gly
 85 90 95

Thr Ala Met Arg Pro Leu Ala Ala Leu Cys Leu Gly Gln Asn Glu
 100 105 110

Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
 115 120 125

Leu Val Asp Ser Leu Arg Gln Gly Gly Ala Asn Ile Asp Tyr Leu Glu
 130 135 140

Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Ile Gly Gly
 145 150 155 160

Asp Ile Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
 165 170 175

Leu Met Thr Ala Pro Leu Ala Pro Glu Asp Thr Ile Ile Arg Val Lys
 180 185 190

Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met
 195 200 205

Lys Thr Phe Gly Val Glu Ile Ala Asn His His Tyr Gln Gln Phe Val
 210 215 220

Val Lys Gly Gly Gln Gln Tyr His Ser Pro Gly Arg Tyr Leu Val Glu
 225 230 235 240

Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Gly Ile Lys
 245 250 255

Gly Gly Thr Val Lys Val Thr Gly Ile Gly Gly Lys Ser Met Gln Gly
 260 265 270

Asp Ile Arg Phe Ala Asp Val Leu His Lys Met Gly Ala Thr Ile Thr
 275 280 285

Trp Gly Asp Asp Phe Ile Ala Cys Thr Arg Gly Glu Leu His Ala Ile
 290 295 300

Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr

305	310	315	320
Thr Ala Leu Phe Ala Lys Gly Thr Thr	Leu Arg Asn Ile Tyr Asn		
325	330	335	
Trp Arg Val Lys Glu Thr Asp Arg	Leu Phe Ala Met Ala Thr Glu Leu		
340	345	350	
Arg Lys Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr	Ile Arg Ile		
355	360	365	
Thr Pro Pro Ala Lys Leu Gln His Ala Asp Ile Gly	Thr Tyr Asn Asp		
370	375	380	
His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp	Thr Pro		
385	390	395	400
Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr			
405	410	415	
Phe Glu Gln Leu Ala Arg Met Ser Thr Pro Ala			
420	425		
<210> 59			
<211> 427			
<212> PRT			
<213> Klebsiella pneumoniae			
<400> 59			
Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Thr Val			
1	5	10	15
Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Ala			
20	25	30	
Ala Leu Ala Arg Gly Thr Thr Val Leu Thr Asn Leu Leu Asp Ser Asp			
35	40	45	
Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Val His Tyr			
50	55	60	
Val Leu Ser Ser Asp Arg Thr Arg Cys Glu Val Thr Gly Thr Gly Gly			
65	70	75	80
Pro Leu Gln Ala Gly Ser Ala Leu Glu Leu Phe Leu Gly Asn Ala Gly			
85	90	95	
Thr Ala Met Arg Pro Leu Ala Ala Leu Cys Leu Gly Ser Asn Asp			
100	105	110	
Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His			
115	120	125	

Leu Val Asp Ala Leu Arg Gln Gly Gly Ala Gln Ile Asp Tyr Leu Glu
130 135 140

Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Thr Gly Gly
145 150 155 160

Asp Val Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
165 170 175

Leu Met Ala Ser Pro Leu Ala Pro Gln Asp Thr Val Ile Ala Ile Lys
180 185 190

Gly Glu Leu Val Ser Arg Pro Tyr Ile Asp Ile Thr Leu His Leu Met
195 200 205

Lys Thr Phe Gly Val Glu Val Glu Asn Gln Ala Tyr Gln Arg Phe Ile
210 215 220

Val Arg Gly Asn Gln Gln Tyr Gln Ser Pro Gly Asp Tyr Leu Val Glu
225 230 235 240

Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Ala Ile Lys
245 250 255

Gly Gly Thr Val Lys Val Thr Gly Ile Gly Arg Asn Ser Val Gln Gly
260 265 270

Asp Ile Arg Phe Ala Asp Val Leu Glu Lys Met Gly Ala Thr Val Thr
275 280 285

Trp Gly Glu Asp Tyr Ile Ala Cys Thr Arg Gly Glu Leu Asn Ala Ile
290 295 300

Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
305 310 315 320

Ala Ala Leu Phe Ala Arg Gly Thr Thr Leu Arg Asn Ile Tyr Asn
325 330 335

Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
340 345 350

Arg Lys Val Gly Ala Glu Val Glu Glu Gly Glu Asp Tyr Ile Arg Ile
355 360 365

Thr Pro Pro Leu Thr Leu Gln Phe Ala Glu Ile Gly Thr Tyr Asn Asp
370 375 380

His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
385 390 395 400

Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
405 410 415

Phe Gly Gln Leu Ala Arg Ile Ser Thr Leu Ala
420 425

<210> 60
<211> 427
<212> PRT
<213> Yersinia enterocolitica

<400> 60

Met Leu Glu Ser Leu Thr Leu His Pro Ile Ala Leu Ile Asn Gly Thr
1 5 10 15

Val Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu
20 25 30

Ala Ala Leu Ala Glu Gly Thr Thr Gln Leu Asn Asn Leu Leu Asp Ser
35 40 45

Asp Asp Ile Arg His Met Leu Asn Ala Leu Gln Ala Leu Gly Val Lys
50 55 60

Tyr Arg Leu Ser Ala Asp Arg Thr Arg Cys Glu Val Asp Gly Leu Gly
65 70 75 80

Gly Lys Leu Val Ala Glu Gln Pro Leu Glu Leu Phe Leu Gly Asn Ala
85 90 95

Gly Thr Ala Met Arg Pro Leu Ala Ala Leu Cys Leu Gly Lys Asn
100 105 110

Asp Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly
115 120 125

His Leu Val Asp Ala Leu Arg Gln Gly Gly Ala Gln Ile Asp Tyr Leu
130 135 140

Glu Gln Glu Asn Tyr Arg Arg Cys Ile Ala Gly Gly Phe Arg Gly Gly
145 150 155 160

Lys Leu Thr Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
165 170 175

Leu Met Thr Ala Pro Leu Ala Glu Gln Asp Thr Glu Ile Gln Ile Gln
180 185 190

Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu His Leu Met
195 200 205

Lys Ala Phe Gly Val Asp Val Val His Glu Asn Tyr Gln Ile Phe His
210 215 220

Ile Lys Gly Gly Gln Thr Tyr Arg Ser Pro Gly Ile Tyr Leu Val Glu
225 230 235 240

Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Ala Ala Ile Lys
245 250 255

Gly Gly Thr Val Arg Val Thr Gly Ile Gly Lys Gln Ser Val Gln Gly
260 265 270

Asp Thr Lys Phe Ala Asp Val Leu Glu Lys Met Gly Ala Lys Ile Ser
275 280 285

Trp Gly Asp Asp Tyr Ile Glu Cys Ser Arg Gly Glu Leu Gln Gly Ile
290 295 300

Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
305 310 315 320

Thr Ala Leu Phe Ala Asp Gly Pro Thr Val Ile Arg Asn Ile Tyr Asn
325 330 335

Trp Arg Val Lys Glu Thr Asp Arg Leu Ser Ala Met Ala Thr Glu Leu
340 345 350

Arg Lys Val Gly Ala Glu Val Glu Glu Gly Gln Asp Tyr Ile Arg Val
355 360 365

Val Pro Pro Ala Gln Leu Ile Ala Ala Glu Ile Gly Thr Tyr Asn Asp
370 375 380

His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
385 390 395 400

Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
405 410 415

Phe Glu Gln Leu Ala Arg Leu Ser Gln Ile Ala
420 425

<210> 61
<211> 432
<212> PRT
<213> *Haemophilus influenzae*

<400> 61

Met Glu Lys Ile Thr Leu Ala Pro Ile Ser Ala Val Glu Gly Thr Ile
1 5 10 15

Asn Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ala Leu Leu Leu Ala
20 25 30

Ala Leu Ala Lys Gly Thr Thr Lys Val Thr Asn Leu Leu Asp Ser Asp
35 40 45

Asp Ile Arg His Met Leu Asn Ala Leu Lys Ala Leu Gly Val Arg Tyr

50 55 60

Gln Leu Ser Asp Asp Lys Thr Ile Cys Glu Ile Glu Gly Leu Gly Gly
65 70 75 80

Ala Phe Asn Ile Gln Asp Asn Leu Ser Leu Phe Leu Gly Asn Ala Gly
85 90 95

Thr Ala Met Arg Pro Leu Thr Ala Ala Leu Cys Leu Lys Gly Asn His
100 105 110

Glu Val Glu Ile Ile Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro
115 120 125

Ile Leu His Leu Val Asp Ala Leu Arg Gln Ala Gly Ala Asp Ile Arg
130 135 140

Tyr Leu Glu Asn Glu Gly Tyr Pro Pro Leu Ala Ile Arg Asn Lys Gly
145 150 155 160

Ile Lys Gly Gly Lys Val Lys Ile Asp Gly Ser Ile Ser Ser Gln Phe
165 170 175

Leu Thr Ala Leu Leu Met Ser Ala Pro Leu Ala Glu Asn Asp Thr Glu
180 185 190

Ile Glu Ile Ile Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr
195 200 205

Leu Ala Met Met Arg Asp Phe Gly Val Lys Val Glu Asn His His Tyr
210 215 220

Gln Lys Phe Gln Val Lys Gly Asn Gln Ser Tyr Ile Ser Pro Asn Lys
225 230 235 240

Tyr Leu Val Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala
245 250 255

Gly Ala Ile Lys Gly Lys Val Lys Val Thr Gly Ile Gly Lys Asn Ser
260 265 270

Ile Gln Gly Asp Arg Leu Phe Ala Asp Val Leu Glu Lys Met Gly Ala
275 280 285

Lys Ile Thr Trp Gly Glu Asp Phe Ile Gln Ala Glu His Ala Glu Leu
290 295 300

Asn Gly Ile Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr
305 310 315 320

Ile Ala Thr Thr Ala Leu Phe Ser Asn Gly Glu Thr Val Ile Arg Asn
325 330 335

Ile Tyr Asn Trp Arg Val Lys Glu Thr Asp Arg Leu Thr Ala Met Ala

340

345

350

Thr Glu Leu Arg Lys Val Gly Ala Glu Val Glu Glu Gly Glu Asp Phe
 355 360 365

Ile Arg Ile Gln Pro Leu Ala Leu Asn Gln Phe Lys His Ala Asn Ile
 370 375 380

Glu Thr Tyr Asn Asp His Arg Met Ala Met Cys Phe Ser Leu Ile Ala
 385 390 395 400

Leu Ser Asn Thr Pro Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys
 405 410 415

Thr Phe Pro Thr Phe Asn Glu Phe Glu Lys Ile Cys Leu Lys Asn
 420 425 430

<210> 62

<211> 441

<212> PRT

<213> Pasteurella multocida

<400> 62

Val Ile Lys Asp Ala Thr Ala Ile Thr Leu Asn Pro Ile Ser Tyr Ile
 1 5 10 15

Glu Gly Glu Val Arg Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ala
 20 25 30

Leu Leu Leu Ser Ala Leu Ala Lys Gly Lys Thr Thr Leu Thr Asn Leu
 35 40 45

Leu Asp Ser Asp Asp Val Arg His Met Leu Asn Ala Leu Lys Glu Leu
 50 55 60

Gly Val Thr Tyr Gln Leu Ser Glu Asp Lys Ser Val Cys Glu Ile Glu
 65 70 75 80

Gly Leu Gly Arg Ala Phe Glu Trp Gln Ser Gly Leu Ala Leu Phe Leu
 85 90 95

Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Leu Cys Leu
 100 105 110

Ser Thr Pro Asn Arg Glu Gly Lys Asn Glu Ile Val Leu Thr Gly Glu
 115 120 125

Pro Arg Met Lys Glu Arg Pro Ile Gln His Leu Val Asp Ala Leu Cys
 130 135 140

Gln Ala Gly Ala Glu Ile Gln Tyr Leu Glu Gln Glu Gly Tyr Pro Pro
 145 150 155 160

Ile Ala Ile Arg Asn Thr Gly Leu Lys Gly Gly Arg Ile Gln Ile Asp
165 170 175

Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu Leu Met Ala Ala Pro
180 185 190

Met Ala Glu Ala Asp Thr Glu Ile Glu Ile Ile Gly Glu Leu Val Ser
195 200 205

Lys Pro Tyr Ile Asp Ile Thr Leu Lys Met Met Gln Thr Phe Gly Val
210 215 220

Glu Val Glu Asn Gln Ala Tyr Gln Arg Phe Leu Val Lys Gly His Gln
225 230 235 240

Gln Tyr Gln Ser Pro His Arg Phe Leu Val Glu Gly Asp Ala Ser Ser
245 250 255

Ala Ser Tyr Phe Leu Ala Ala Ala Ile Lys Gly Lys Val Lys Val
260 265 270

Thr Gly Val Gly Lys Asn Ser Ile Gln Gly Asp Arg Leu Phe Ala Asp
275 280 285

Val Leu Glu Lys Met Gly Ala His Ile Thr Trp Gly Asp Asp Phe Ile
290 295 300

Gln Val Glu Lys Gly Asn Leu Lys Gly Ile Asp Met Asp Met Asn His
305 310 315 320

Ile Pro Asp Ala Ala Met Thr Ile Ala Thr Thr Ala Leu Phe Ala Glu
325 330 335

Gly Glu Thr Val Ile Arg Asn Ile Tyr Asn Trp Arg Val Lys Glu Thr
340 345 350

Asp Arg Leu Thr Ala Met Ala Thr Glu Leu Arg Lys Val Gly Ala Glu
355 360 365

Val Glu Glu Gly Glu Asp Phe Ile Arg Ile Gln Pro Leu Asn Leu Ala
370 375 380

Gln Phe Gln His Ala Glu Leu Asn Ile His Asp His Arg Met Ala Met
385 390 395 400

Cys Phe Ala Leu Ile Ala Leu Ser Lys Thr Ser Val Thr Ile Leu Asp
405 410 415

Pro Ser Cys Thr Ala Lys Thr Phe Pro Thr Phe Leu Ile Leu Phe Thr
420 425 430

Leu Asn Thr Arg Glu Val Ala Tyr Arg
435 440

<210> 63
<211> 426
<212> PRT
<213> Aeromonas salmonicida

<400> 63

Asn Ser Leu Arg Leu Glu Pro Ile Ser Arg Val Ala Gly Glu Val Asn
1 5 10 15

Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala Ala
20 25 30

Leu Ala Arg Gly Thr Thr Arg Leu Thr Asn Leu Leu Asp Ser Asp Asp
35 40 45

Ile Arg His Met Leu Ala Ala Leu Thr Gln Leu Gly Val Lys Tyr Lys
50 55 60

Leu Ser Ala Asp Lys Thr Glu Cys Thr Val His Gly Leu Gly Arg Ser
65 70 75 80

Phe Ala Val Ser Ala Pro Val Asn Leu Phe Leu Gly Asn Ala Gly Thr
85 90 95

Ala Met Arg Pro Leu Cys Ala Ala Leu Cys Leu Gly Ser Gly Glu Tyr
100 105 110

Met Leu Gly Gly Glu Pro Arg Met Glu Glu Arg Pro Ile Gly His Leu
115 120 125

Val Asp Cys Leu Ala Leu Lys Gly Ala His Ile Gln Tyr Leu Lys Lys
130 135 140

Asp Gly Tyr Pro Pro Leu Val Val Asp Ala Lys Gly Leu Trp Gly Gly
145 150 155 160

Asp Val His Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Phe
165 170 175

Leu Met Ala Ala Pro Ala Met Ala Pro Val Ile Pro Arg Ile His Ile
180 185 190

Lys Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu His Ile
195 200 205

Met Asn Ser Ser Gly Val Val Ile Glu His Asp Asn Tyr Lys Leu Phe
210 215 220

Tyr Ile Lys Gly Asn Gln Ser Ile Val Ser Pro Gly Asp Phe Leu Val
225 230 235 240

Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Ala Ile
245 250 255

Lys Gly Lys Val Arg Val Thr Gly Ile Gly Lys His Ser Ile Gly Asp
260 265 270

Ile His Phe Ala Asp Val Leu Glu Arg Met Gly Ala Arg Ile Thr Trp
275 280 285

Gly Asp Asp Phe Ile Glu Ala Glu Gln Gly Pro Leu His Gly Val Asp
290 295 300

Met Asp Met Asn His Ile Pro Asp Val Gly His Asp His Ser Gly Gln
305 310 315 320

Ser His Cys Leu Pro Arg Val Pro Pro His Ser Gln His Leu Gln Leu
325 330 335

Ala Val Arg Asp Asp Arg Cys Thr Pro Cys Thr His Gly His Arg Arg
340 345 350

Ala Gln Ala Gly Val Ser Glu Glu Gly Thr Thr Phe Ile Thr Arg Asp
355 360 365

Ala Ala Asp Pro Ala Gln Ala Arg Arg Asp Arg His Leu Gln Arg Ser
370 375 380

Arg Ile Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Ile Ala Val
385 390 395 400

Thr Ile Asn Asp Pro Gly Cys Thr Ser Lys Thr Phe Pro Asp Tyr Phe
405 410 415

Asp Lys Leu Ala Ser Val Ser Gln Ala Val
420 425

<210> 64

<211> 442

<212> PRT

<213> *Bacillus pertussis*

<400> 64

Met Ser Gly Leu Ala Tyr Leu Asp Leu Pro Ala Ala Arg Leu Ala Arg
1 5 10 15

Gly Glu Val Ala Leu Pro Gly Ser Lys Ser Ile Ser Asn Arg Val Leu
20 25 30

Leu Leu Ala Ala Leu Ala Glu Gly Ser Thr Glu Ile Thr Gly Leu Leu
35 40 45

Asp Ser Asp Asp Thr Arg Val Met Leu Ala Ala Leu Arg Gln Leu Gly
50 55 60

Val Ser Val Gly Glu Val Ala Asp Gly Cys Val Thr Ile Glu Gly Val

65

70

75

80

Ala Arg Phe Pro Thr Glu Gln Ala Glu Leu Phe Leu Gly Asn Ala Gly
85 . 90 . 95

Thr Ala Phe Arg Pro Leu Thr Ala Ala Leu Ala Leu Met Gly Gly Asp
100 . 105 . 110

Tyr Arg Leu Ser Gly Val Pro Arg Met His Glu Arg Pro Ile Gly Asp
115 . 120 . 125

Leu Val Asp Ala Leu Arg Gln Phe Gly Ala Gly Ile Glu Tyr Leu Gly
130 . 135 . 140

Gln Ala Gly Tyr Pro Pro Leu Arg Ile Gly Gly Ser Ile Arg Val
145 . 150 . 155 . 160

Asp Gly Pro Val Arg Val Glu Gly Ser Val Ser Ser Gln Phe Leu Thr
165 . 170 . 175

Ala Leu Leu Met Ala Ala Pro Val Leu Ala Arg Arg Ser Gly Gln Asp
180 . 185 . 190

Ile Thr Ile Glu Val Val Gly Glu Leu Ile Ser Lys Pro Tyr Ile Glu
195 . 200 . 205

Ile Thr Leu Asn Leu Met Ala Arg Phe Gly Val Ser Val Arg Arg Asp
210 . 215 . 220

Gly Trp Arg Ala Phe Thr Ile Ala Arg Asp Ala Val Tyr Arg Gly Pro
225 . 230 . 235 . 240

Gly Arg Met Ala Ile Glu Gly Asp Ala Ser Thr Ala Ser Tyr Phe Leu
245 . 250 . 255

Ala Leu Gly Ala Ile Gly Gly Pro Val Arg Val Thr Gly Val Gly
260 . 265 . 270

Glu Asp Ser Ile Gln Gly Asp Val Ala Phe Ala Ala Thr Leu Ala Ala
275 . 280 . 285

Met Gly Ala Asp Val Arg Tyr Gly Pro Gly Trp Ile Glu Thr Arg Gly
290 . 295 . 300

Val Arg Val Ala Glu Gly Gly Arg Leu Lys Ala Phe Asp Ala Asp Phe
305 . 310 . 315 . 320

Asn Leu Ile Pro Asp Ala Ala Met Thr Ala Ala Thr Leu Ala Leu Tyr
325 . 330 . 335

Ala Asp Gly Pro Cys Arg Leu Arg Asn Ile Gly Ser Trp Arg Val Lys
340 . 345 . 350

Glu Thr Asp Arg Ile His Ala Met His Thr Glu Leu Glu Lys Leu Gly

355

360

365

Ala Gly Val Gln Ser Gly Ala Asp Trp Leu Glu Val Ala Pro Pro Glu
370 375 380

Pro Gly Gly Trp Arg Asp Ala His Ile Gly Thr Trp Asp Asp His Arg
385 390 395 400

Met Ala Met Cys Phe Leu Leu Ala Ala Phe Gly Pro Ala Ala Val Arg
405 410 415

Ile Leu Asp Pro Gly Cys Val Ser Lys Thr Phe Pro Asp Tyr Phe Asp
420 425 430

Val Tyr Ala Gly Leu Leu Ala Ala Arg Asp
435 440

<210> 65

<211> 427

<212> PRT

<213> *Salmonella typhimurium*

<400> 65

Met Glu Ser Leu Thr Leu Gln Pro Ile Ala Arg Val Asp Gly Ala Ile
1 5 10 15

Asn Leu Pro Gly Ser Lys Ser Val Ser Asn Arg Ala Leu Leu Leu Ala
20 25 30

Ala Leu Ala Cys Gly Lys Thr Val Leu Thr Asn Leu Leu Asp Ser Asp
35 40 45

Asp Val Arg His Met Leu Asn Ala Leu Ser Ala Leu Gly Ile Asn Tyr
50 55 60

Thr Leu Ser Ala Asp Arg Thr Arg Cys Asp Ile Thr Gly Asn Gly Gly
65 70 75 80

Pro Leu Arg Ala Ser Gly Thr Leu Glu Leu Phe Leu Gly Asn Ala Gly
85 90 95

Thr Ala Met Arg Pro Leu Ala Ala Leu Cys Leu Gly Gln Asn Glu
100 105 110

Ile Val Leu Thr Gly Glu Pro Arg Met Lys Glu Arg Pro Ile Gly His
115 120 125

Leu Val Asp Ser Leu Arg Gln Gly Gly Ala Asn Ile Asp Tyr Leu Glu
130 135 140

Gln Glu Asn Tyr Pro Pro Leu Arg Leu Arg Gly Gly Phe Ile Gly Gly
145 150 155 160

Asp Ile Glu Val Asp Gly Ser Val Ser Ser Gln Phe Leu Thr Ala Leu
165 170 175

Leu Met Thr Ala Pro Leu Ala Pro Glu Asp Thr Ile Ile Arg Val Lys
180 185 190

Gly Glu Leu Val Ser Lys Pro Tyr Ile Asp Ile Thr Leu Asn Leu Met
195 200 205

Lys Thr Phe Gly Val Glu Ile Ala Asn His His Tyr Gln Gln Phe Val
210 215 220

Val Lys Gly Gly Gln Gln Tyr His Ser Pro Gly Arg Tyr Leu Val Glu
225 230 235 240

Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Ala Gly Gly Ile Lys
245 250 255

Gly Gly Thr Val Lys Val Thr Gly Ile Gly Gly Lys Ser Met Gln Gly
260 265 270

Asp Ile Arg Phe Ala Asp Val Leu His Lys Met Gly Ala Thr Ile Thr
275 280 285

Trp Gly Asp Asp Phe Ile Ala Cys Thr Arg Gly Glu Leu His Ala Ile
290 295 300

Asp Met Asp Met Asn His Ile Pro Asp Ala Ala Met Thr Ile Ala Thr
305 310 315 320

Thr Ala Leu Phe Ala Lys Gly Thr Thr Leu Arg Asn Ile Tyr Asn
325 330 335

Trp Arg Val Lys Glu Thr Asp Arg Leu Phe Ala Met Ala Thr Glu Leu
340 345 350

Arg Lys Val Gly Ala Glu Val Glu Glu Gly His Asp Tyr Ile Arg Ile
355 360 365

Thr Pro Pro Ala Lys Leu Gln His Ala Asp Ile Gly Thr Tyr Asn Asp
370 375 380

His Arg Met Ala Met Cys Phe Ser Leu Val Ala Leu Ser Asp Thr Pro
385 390 395 400

Val Thr Ile Leu Asp Pro Lys Cys Thr Ala Lys Thr Phe Pro Asp Tyr
405 410 415

Phe Glu Gln Leu Ala Arg Met Ser Thr Pro Ala
420 425

<210> 66
<211> 1894
<212> DNA

<213> Synechocystis sp.

<220>

<221> CDS

<222> (275)..(1618)

<400> 66
acgggctgta acggtagtag gggtcccgag cacaaaagcg gtgcggcaa gcagaactaa 60
tttccatggg gaataatggt atttcattgg tttggcctct ggtctggcaa tggttgctag 120
gcgatcgct gttgaaattha acaaactgtc gcccttccac tgaccatggt aacgatgtt 180
tttacttcct tgactaaccg aggaaaattt ggccgggggc agaaatgccaa atacaattt 240
gcttggtctt ccctgccccct aatttgcctt ctcc atg gcc ttg ctt tcc ctc aac 295
Met Ala Leu Leu Ser Leu Asn
1 5
aat cat caa tcc cat caa cgc tta act gtt aat ccc cct gcc caa ggg 343
Asn His Gln Ser His Gln Arg Leu Thr Val Asn Pro Pro Ala Gln Gly
10 15 20
gtc gct ttg act ggc cgc cta agg gtg ccg ggg gat aaa tcc att tcc 391
Val Ala Leu Thr Gly Arg Leu Arg Val Pro Gly Asp Lys Ser Ile Ser
25 30 35
cat cgg gcc ttg atg ttg ggg gcg atc gcc acc ggg gaa acc att atc 439
His Arg Ala Leu Met Leu Gly Ala Ile Ala Thr Gly Glu Thr Ile Ile
40 45 50 55
gaa ggg cta ctg ttg ggg gaa gat ccc cgt agt acg gcc cat tgc ttt 487
Glu Gly Leu Leu Leu Gly Glu Asp Pro Arg Ser Thr Ala His Cys Phe
60 65 70
cgg gcc atg gga gca gaa atc agc gaa cta aat tca gaa aaa atc atc 535
Arg Ala Met Gly Ala Glu Ile Ser Glu Leu Asn Ser Glu Lys Ile Ile
75 80 85
gtt cag ggt cgg ggt ctg gga cag ttg cag gaa ccc agt acc gtt ttg 583
Val Gln Gly Arg Gly Leu Gly Gln Leu Gln Glu Pro Ser Thr Val Leu
90 95 100
gat gcg ggg aac tct ggc acc acc atg cgc tta atg ttg ggc ttg cta 631
Asp Ala Gly Asn Ser Gly Thr Thr Met Arg Leu Met Leu Gly Leu Leu
105 110 115
gcc ggg caa aaa gat tgt tta ttc acc gtc acc ggc gat gat tcc ctc 679
Ala Gly Gln Lys Asp Cys Leu Phe Thr Val Thr Gly Asp Asp Ser Leu
120 125 130 135
cgt cac cgc ccc atg tcc cgg gta att caa ccc ttg caa caa atg ggg 727
Arg His Arg Pro Met Ser Arg Val Ile Gln Pro Leu Gln Gln Met Gly
140 145 150

gca aaa att tgg gcc cg ^g agt aac gg ^c aag ttt gc ^g cc ^g ct ^g gca gtc Ala Lys Ile Trp Ala Arg Ser Asn Gly Lys Phe Ala Pro Leu Ala Val 155 160 165	775
cag ggt agc c ^a tta aaa cc ^g atc cat tac cat tcc ccc att gct tca Gln Gly Ser Gln Leu Lys Pro Ile His Tyr His Ser Pro Ile Ala Ser 170 175 180	823
gcc cag gta aag tcc tgc ct ^g tt ^g cta gc ^g ggg tta acc acc gag ggg Ala Gln Val Lys Ser Cys Leu Leu Leu Ala Gly Leu Thr Thr Glu Gly 185 190 195	871
gac acc acg gtt aca gaa cca gct cta tcc cg ^g gat cat agc gaa cg ^c Asp Thr Thr Val Thr Glu Pro Ala Leu Ser Arg Asp His Ser Glu Arg 200 205 210 215	919
atg ttg cag gcc ttt gga gcc aaa tta acc att gat cca gta acc cat Met Leu Gln Ala Phe Gly Ala Lys Leu Thr Ile Asp Pro Val Thr His 220 225 230	967
agc gtc act gtc cat gg ^c cc ^g gc ^c cat tta ac ^g ggg caa cg ^g gt ^g gt ^g Ser Val Thr Val His Gly Pro Ala His Leu Thr Gly Gln Arg Val Val 235 240 245	1015
gt ^g cca ggg gac atc agc tc ^g gc ^g gc ^c ttt tgg tta gt ^g gc ^g gca tcc Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Trp Leu Val Ala Ala Ser 250 255 260	1063
att ttg cct gga tca gaa ttg ttg gt ^g gaa aat gta gg ^c att aac ccc Ile Leu Pro Gly Ser Glu Leu Leu Val Glu Asn Val Gly Ile Asn Pro 265 270 275	1111
acc agg aca ggg gt ^g tt ^g gaa gt ^g tt ^g gc ^c cag at ^g ggg gc ^g gac att Thr Arg Thr Gly Val Leu Glu Val Leu Ala Gln Met Gly Ala Asp Ile 280 285 290 295	1159
acc ccg gag aat gaa cga tt ^g gta ac ^g ggg gaa cc ^g gta gca gat ct ^g Thr Pro Glu Asn Glu Arg Leu Val Thr Gly Glu Pro Val Ala Asp Leu 300 305 310	1207
cg ^g gtt agg gca agc cat ctc cag ggt tgc acc ttc gg ^c gg ^c gaa att Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly Glu Ile 315 320 325	1255
att ccc cga ct ^g att gat gaa att ccc att tt ^g gca gt ^g gc ^g gc ^c Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Leu Ala Val Ala Ala 330 335 340	1303
ttt gca gag gg ^c act acc cg ^c att gaa gat gc ^c gca gaa ct ^g agg gtt Phe Ala Glu Gly Thr Thr Arg Ile Glu Asp Ala Ala Glu Leu Arg Val 345 350 355	1351
aaa gaa agc gat cg ^c ct ^g gc ^g gc ^c att gct tc ^g gag tt ^g gg ^c aaa at ^g	1399



Lys Glu Ser Asp Arg Leu Ala Ala Ile Ala Ser Glu Leu Gly Lys Met				
360	365	370	375	
ggg gcc aaa gtc acc gaa ttt gat gat ggc ctg gaa att caa ggg gga				1447
Gly Ala Lys Val Thr Glu Phe Asp Asp Gly Leu Glu Ile Gln Gly Gly				
380	385	390		
agc ccg tta caa ggg gcc gag gtg gat agc ttg acg gat cat cgc att				1495
Ser Pro Leu Gln Gly Ala Glu Val Asp Ser Leu Thr Asp His Arg Ile				
395	400	405		
gcc atg gcg ttg gcg atc gcc gct tta ggt agt ggg ggg caa aca att				1543
Ala Met Ala Leu Ala Ile Ala Ala Leu Gly Ser Gly Gly Gln Thr Ile				
410	415	420		
att aac cgg gcg gaa gcg gcc gcc att tcc tat cca gaa ttt ttt ggc				1591
Ile Asn Arg Ala Glu Ala Ala Ile Ser Tyr Pro Glu Phe Phe Gly				
425	430	435		
acg cta ggg caa gtt gcc caa gga taa agtttagaaaa actcctggc				1638
Thr Leu Gly Gln Val Ala Gln Gly				
440	445			
ggtttgtaaa tggtttacca aggttagttt gggtaaaggc cccagcaagt gctgccaggg				1698
taatttatcc gcaattgacc aatcggcatg gaccgtatcg ttcaaaactgg gtaattctcc				1758
ctttaattcc ttaaaagctc gcttaaaact gcccaacgta tctccgtaat ggcgagttag				1818
tagaagtaat gggccaaac ggcgatcgcc acggaaatt aaaggctgca tcactgacca				1878
cttataactt tcggga				1894

<210> 67
 <211> 447
 <212> PRT
 <213> *Synechocystis* sp.

<400> 67

Met Ala Leu Leu Ser Leu Asn Asn His Gln Ser His Gln Arg Leu Thr			
1	5	10	15

Val Asn Pro Pro Ala Gln Gly Val Ala Leu Thr Gly Arg Leu Arg Val			
20	25	30	

Pro Gly Asp Lys Ser Ile Ser His Arg Ala Leu Met Leu Gly Ala Ile			
35	40	45	

Ala Thr Gly Glu Thr Ile Ile Glu Gly Leu Leu Gly Glu Asp Pro

50

55

60

Arg Ser Thr Ala His Cys Phe Arg Ala Met Gly Ala Glu Ile Ser Glu
65 70 75 80

Leu Asn Ser Glu Lys Ile Ile Val Gln Gly Arg Gly Leu Gly Gln Leu
85 90 95

Gln Glu Pro Ser Thr Val Leu Asp Ala Gly Asn Ser Gly Thr Thr Met
100 105 110

Arg Leu Met Leu Gly Leu Leu Ala Gly Gln Lys Asp Cys Leu Phe Thr
115 120 125

Val Thr Gly Asp Asp Ser Leu Arg His Arg Pro Met Ser Arg Val Ile
130 135 140

Gln Pro Leu Gln Gln Met Gly Ala Lys Ile Trp Ala Arg Ser Asn Gly
145 150 155 160

Lys Phe Ala Pro Leu Ala Val Gln Gly Ser Gln Leu Lys Pro Ile His
165 170 175

Tyr His Ser Pro Ile Ala Ser Ala Gln Val Lys Ser Cys Leu Leu Leu
180 185 190

Ala Gly Leu Thr Thr Glu Gly Asp Thr Thr Val Thr Glu Pro Ala Leu
195 200 205

Ser Arg Asp His Ser Glu Arg Met Leu Gln Ala Phe Gly Ala Lys Leu
210 215 220

Thr Ile Asp Pro Val Thr His Ser Val Thr Val His Gly Pro Ala His
225 230 235 240

Leu Thr Gly Gln Arg Val Val Val Pro Gly Asp Ile Ser Ser Ala Ala
245 250 255

Phe Trp Leu Val Ala Ala Ser Ile Leu Pro Gly Ser Glu Leu Leu Val
260 265 270

Glu Asn Val Gly Ile Asn Pro Thr Arg Thr Gly Val Leu Glu Val Leu
275 280 285

Ala Gln Met Gly Ala Asp Ile Thr Pro Glu Asn Glu Arg Leu Val Thr
290 295 300

Gly Glu Pro Val Ala Asp Leu Arg Val Arg Ala Ser His Leu Gln Gly
305 310 315 320

Cys Thr Phe Gly Gly Glu Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro
325 330 335

Ile Leu Ala Val Ala Ala Ala Phe Ala Glu Gly Thr Thr Arg Ile Glu
340 345 350

Asp Ala Ala Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Ile
355 360 365

Ala Ser Glu Leu Gly Lys Met Gly Ala Lys Val Thr Glu Phe Asp Asp
370 375 380

Gly Leu Glu Ile Gln Gly Gly Ser Pro Leu Gln Gly Ala Glu Val Asp
385 390 395 400

Ser Leu Thr Asp His Arg Ile Ala Met Ala Leu Ala Ile Ala Ala Leu
405 410 415

Gly Ser Gly Gly Gln Thr Ile Ile Asn Arg Ala Glu Ala Ala Ala Ile
420 425 430

Ser Tyr Pro Glu Phe Phe Gly Thr Leu Gly Gln Val Ala Gln Gly
435 440 445

<210> 68
<211> 1479
<212> DNA
<213> *Dichelobacter nodosus*

<220>
<221> CDS
<222> (107)...(1438)

<400> 68
 tttaaaaaca atgagttaaa aaattatttt tctggcacac gcgcgttttt tgcattttt 60
 ctcccatttt tccggcacaa taacgttggg tttataaaag gaaatg atg atg acg
 Met Met Thr
 1

aat ata tgg cac acc gcg ccc gtc tct gcg ctt tcc ggc gaa ata acg 163
 Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly Glu Ile Thr
 5 10 15

ata tgc ggc gat aaa tca atg tcg cat cgc gcc tta tta tta gca gcg 211
 Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu Leu Ala Ala
 20 25 30 35

tta gca gaa gga caa acg gaa atc cgc ggc ttt tta gcg tgc gcg gat 259
 Leu Ala Glu Gly Gln Thr Glu Ile Arg Gly Phe Leu Ala Cys Ala Asp
 40 45 50

tgt ttg gcg acg cgg caa gca ttg cgc gca tta ggc gtt gat att caa 307
 Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val Asp Ile Gln
 55 60 65

aga gaa aaa gaa ata gtg acg att cgc ggt gtg gga ttt ctg ggt ttg 355
 Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe Leu Gly Leu
 70 75 80

cag ccg ccg aaa gca ccg tta aat atg caa aac agt ggc act agc atg 403
 Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly Thr Ser Met
 85 90 95

cgt tta ttg gca gga att ttg gca gcg cag cgc ttt gag agc gtg tta 451
 Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu Ser Val Leu
 100 105 110 115

tgc ggc gat gaa tca tta gaa aaa cgt ccg atg cag cgc att att acg 499
 Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg Ile Ile Thr
 120 125 130

ccg ctt gtg caa atg ggg gca aaa att gtc agt cac agc aat ttt acg 547
 Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser Asn Phe Thr
 135 140 145

gcg ccg tta cat att tca gga cgc ccg ctg acc ggc att gat tac gcg 595
 Ala Pro Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile Asp Tyr Ala
 150 155 160

tta ccg ctt ccc agc gcg caa tta aaa agt tgc ctt att ttg gca gga 643
 Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile Leu Ala Gly
 165 170 175

tta ttg gct gac ggt acc acg cgg ctg cat act tgc ggc atc agt cgc 691
 Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly Ile Ser Arg
 180 185 190 195

gac cac acg gaa cgc atg ttg ccg ctt ttt ggt ggc gca ctt gag atc Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala Leu Glu Ile 200	205	210	739	
aag aaa gag caa ata atc gtc acc ggt gga caa aaa ttg cac ggt tgc Lys Lys Glu Gln Ile Ile Val Thr Gly Gly Gln Lys Leu His Gly Cys 215	220	225	787	
gtg ctt gat att gtc ggc gat ttg tcg gcg gcg ttt ttt atg gtt Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Phe Phe Met Val 230	235	240	835	
gcg gct ttg att gcg ccg cgc gcg gaa gtc gtt att cgt aat gtc ggc Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Val Ile Arg Asn Val Gly 245	250	255	883	
att aat ccg acg cgg gcg gca atc att act ttg ttg caa aaa atg ggc Ile Asn Pro Thr Arg Ala Ala Ile Ile Thr Leu Leu Gln Lys Met Gly 260	265	270	275	931
gga cgg att gaa ttg cat cat cag cgc ttt tgg ggc gcc gaa ccg gtc Gly Arg Ile Glu Leu His His Gln Arg Phe Trp Gly Ala Glu Pro Val 280	285	290	979	
gca gat att gtt gtt tat cat tca aaa ttg cgc ggc att acg gtc gcg Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile Thr Val Ala 295	300	305	1027	
ccg gaa tgg att gcc aac gcg att gat gaa ttg ccg att ttt ttt att Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile Phe Phe Ile 310	315	320	1075	
gcg gca gct tgc gcg gaa ggg acg act ttt gtc ggc aat ttg tca gaa Ala Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn Leu Ser Glu 325	330	335	1123	
ttg cgt gtc aaa gaa tcg gat cgt tta gcg gcg atg gcg caa aat tta Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala Gln Asn Leu 340	345	350	355	1171
caa act ttg ggc gtc gcg tgc gac gtt ggc gcc gat ttt att cat ata Gln Thr Leu Gly Val Ala Cys Asp Val Gly Ala Asp Phe Ile His Ile 360	365	370	1219	
tat gga aga agc gat cgg caa ttt tta ccg gcg cgg gtc aac agt ttt Tyr Gly Arg Ser Asp Arg Gln Phe Leu Pro Ala Arg Val Asn Ser Phe 375	380	385	1267	
ggc gat cat cgg att gcg atg agt ttg gcg gtc gca ggt gtc cgc gcg Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly Val Arg Ala 390	395	400	1315	
gca ggt gaa tta ttg att gat gac ggc gcg gtc gcg gtt tct atg			1363	

Ala Gly Glu Leu Leu Ile Asp Asp Gly Ala Val Ala Ala Val Ser Met
405 410 415

ccg caa ttt cgc gat ttt gcc gcc gca att ggt atg aat gta gga gaa 1411
Pro Gln Phe Arg Asp Phe Ala Ala Ala Ile Gly Met Asn Val Gly Glu
420 425 430 435

aaa gat gcg aaa aat tgt cac gat tga tggtcctagc ggtgttggaa 1458
Lys Asp Ala Lys Asn Cys His Asp
440

aaggcacggt ggcgcaagct t 1479

<210> 69
<211> 443
<212> PRT
<213> Dichelobacter nodosus

<400> 69

Met Met Thr Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly
1 5 10 15

Glu Ile Thr Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu
20 25 30

Leu Ala Ala Leu Ala Glu Gly Gln Thr Glu Ile Arg Gly Phe Leu Ala
35 40 45

Cys Ala Asp Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val
50 55 60

Asp Ile Gln Arg Glu Lys Glu Ile Val Thr Ile Arg Gly Val Gly Phe
65 70 75 80

Leu Gly Leu Gln Pro Pro Lys Ala Pro Leu Asn Met Gln Asn Ser Gly
85 90 95

Thr Ser Met Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu
100 105 110

Ser Val Leu Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg
115 120 125

Ile Ile Thr Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser

130 135 140

Asn Phe Thr Ala Pro Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile
145 150 155 160

Asp Tyr Ala Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile
165 170 175

Leu Ala Gly Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly
180 185 190

Ile Ser Arg Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala
195 200 205

Leu Glu Ile Lys Lys Glu Gln Ile Ile Val Thr Gly Gly Gln Lys Leu
210 215 220

His Gly Cys Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Ala Phe
225 230 235 240

Phe Met Val Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Val Ile Arg
245 250 255

Asn Val Gly Ile Asn Pro Thr Arg Ala Ala Ile Ile Thr Leu Leu Gln
260 265 270

Lys Met Gly Gly Arg Ile Glu Leu His His Gln Arg Phe Trp Gly Ala
275 280 285

Glu Pro Val Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile
290 295 300

Thr Val Ala Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile
305 310 315 320

Phe Phe Ile Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn
325 330 335

Leu Ser Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala
340 345 350

77 184

AT

Gln Asn Leu Gln Thr Leu Gly Val Ala Cys Asp Val Gly Ala Asp Phe
355 360 365

Ile His Ile Tyr Gly Arg Ser Asp Arg Gln Phe Leu Pro Ala Arg Val
370 375 380

Asn Ser Phe Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly
385 390 395 400

Val Arg Ala Ala Gly Glu Leu Leu Ile Asp Asp Gly Ala Val Ala Ala
405 410 415

Val Ser Met Pro Gln Phe Arg Asp Phe Ala Ala Ala Ile Gly Met Asn
420 425 430

Val Gly Glu Lys Asp Ala Lys Asn Cys His Asp
435 440

<210> 70

<211> 455

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic

<400> 70

Met Leu His Gly Ala Ser Ser Arg Pro Ala Thr Ala Arg Lys Ser Ser
1 5 10 15

Gly Leu Ser Gly Thr Val Arg Ile Pro Gly Asp Lys Ser Ile Ser His
20 25 30

Arg Ser Phe Met Phe Gly Gly Leu Ala Ser Gly Glu Thr Arg Ile Thr
35 40 45

Gly Leu Leu Glu Gly Glu Asp Val Ile Asn Thr Gly Lys Ala Met Gln
50 55 60

Ala Met Gly Ala Arg Ile Arg Lys Glu Gly Asp Thr Trp Ile Ile Asp
65 70 75 80

Gly Val Gly Asn Gly Gly Leu Leu Ala Pro Glu Ala Pro Leu Asp Phe
85 90 95

Gly Asn Ala Ala Thr Gly Cys Arg Leu Thr Met Gly Leu Val Gly Val

100

105

110

Tyr Asp Phe Asp Ser Thr Phe Ile Gly Asp Ala Ser Leu Thr Lys Arg
115 120 125

Pro Met Gly Arg Val Leu Asn Pro Leu Arg Glu Met Gly Val Gln Val
130 135 140

Lys Ser Glu Asp Gly Asp Arg Leu Pro Val Thr Leu Arg Gly Pro Lys
145 150 155 160

Thr Pro Thr Pro Ile Thr Tyr Arg Val Pro Met Ala Ser Ala Gln Val
165 170 175

Lys Ser Ala Val Leu Leu Ala Gly Leu Asn Thr Pro Gly Ile Thr Thr
180 185 190

Val Ile Glu Pro Ile Met Thr Arg Asp His Thr Glu Lys Met Leu Gln
195 200 205

Gly Phe Gly Ala Asn Leu Thr Val Glu Thr Asp Ala Asp Gly Val Arg
210 215 220

Thr Ile Arg Leu Glu Gly Arg Gly Lys Leu Thr Gly Gln Val Ile Asp
225 230 235 240

Val Pro Gly Asp Pro Ser Ser Thr Ala Phe Pro Leu Val Ala Ala Leu
245 250 255

Leu Val Pro Gly Ser Asp Val Thr Ile Leu Asn Val Leu Met Asn Pro
260 265 270

Thr Arg Thr Gly Leu Ile Leu Thr Leu Gln Glu Met Gly Ala Asp Ile
275 280 285

Glu Val Ile Asn Pro Arg Leu Ala Gly Gly Glu Asp Val Ala Asp Leu
290 295 300

Arg Val Arg Ser Ser Thr Leu Lys Gly Val Thr Val Pro Glu Asp Arg
305 310 315 320

Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala Ala
325 330 335

Phe Ala Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg Val
340 345 350

Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu Asn
355 360 365

Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly Arg
370 375 380

Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala Thr

385

390

395

400

His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu Val
405 410 415

Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr Ser
420 425 430

Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile Glu
435 440 445

Leu Ser Asp Thr Lys Ala Ala
450 455

cont.

80 | 87